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SEARCH REQUEST FORM

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Please provide a detailed statement of th	e search topic, and	describe as specifically as possible the subj	ect matter	to be searched
utility of the invention. Define any term	is that may have a s	ms, acronyms, and registry numbers, and cospecial meaning. Give examples or relevant	ombine wit t citations,	h the concept authors, etc. i
known. Please attach a copy of the cover	r sheet, pertinent cl	aims, and abstract.		
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Inventors (please provide full names):				7
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	<u>S440</u>	<u>U</u>	USPT,PGPB	(endoglin same antibod\$) same monoclonal	2001-11-09 15:39:06	
4	<u>S439</u>	<u>U</u>	USPT,PGPB	endoglin same antibod\$	2001-11-09 15:38:39	
)	<u>S438</u>	<u>U</u>	USPT,PGPB	((TGF) adj beta adj binding adj protein) same antibod\$	2001-11-09 15:33:19	
	<u>S437</u>	<u>U</u>	USPT,PGPB	(TGF) adj beta adj binding adj protein	2001-11-09 15:32:52	
	<u>S436</u>	<u>U</u>	USPT	5\$89375.pn.	2001-11-09 15:31:35	
	<u>S435</u>	<u>U</u>	USPT	(((protein adj tyrosine adj phosphatase) same antibod\$)and @py<1997) and claim	2001-11-09 12:58:12	
	<u>S434</u>	<u>U</u>	USPT	((protein adj tyrosine adj phosphatase) same antibod\$) and @py<1999	2001-11-09 12:56:42	
	<u>S433</u>	<u>U</u>	USPT	((protein adj tyrosine adj phosphatase) same antibod\$) and @py<1997	2001-11-09 12:24:41	
	<u>S432</u>	<u>U</u>	USPT	(protein adj tyrosine adj phosphatase) same antibod\$	2001-11-09 12:24:12	
	<u>S431</u>	<u>U</u>	USPT	5580742.pn.	2001-11-09 12:07:49	
	<u>S430</u>	<u>U</u>	USPT	(antibody same phosphotyrosine same phosphatase) and @py<1997	2001-11-09 11:59:41	
	<u>S429</u>	<u>U</u>	USPT	antibody same phosphotyrosine same phosphatase	2001-11-09 11:59:24	
	<u>S428</u>	<u>U</u>	USPT	(antibody same phosphotyrosine same (kinase or phosphatase)) and @py<1997	2001-11-09 11:58:53	
	<u>S427</u>	<u>U</u>	USPT	(antibody same phosphotyrosine same (kinase or phosphatase) same @py<1997	2001-11-09 11:58:42	
	<u>S426</u>	<u>U</u>	USPT	antibody same phosphotyrosine same (kinase or phosphatase)	2001-11-09 11:57:52	
	<u>S425</u>	<u>U</u>	USPT	5863781.pn.	2001-11-09 10:22:54	



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12 467.8 20.3 532 21 AAA29060 BOV1 13 422 18.3 1104 21 AAA29063 Huma 14 372.2 16.2 35828 21 AAA29063 Muri 15 193.8 8.4 198 20 AAX40842 Huma 16 193.4 8.4 196 21 AAA29063 Huma 17 100.4 4.4 936 22 AAF58257 Olig 18 100.4 4.4 936 22 AAF58257 Olig 20 100.4 4.4 936 22 AAF58257 Olig 21 100.4 4.4 936 22 AAF58257 Olig 21 100.4 4.4 936 22 AAF58252 Olig 22 100.4 4.4 936 22 AAF58252 Olig 23 98.6 4.3 936 22 AAF58252 Olig 24 98.6 4.3 936 22 AAF58252 Olig 25 98.6 4.3 936 22 AAF58252 Olig 26 98.6 4.3 936 22 AAF58252 Olig 27 98.6 4.3 936 22 AAF58252 Olig 28 98.6 4.3 936 22 AAF58252 Olig 29 82.6 3.6 954 22 AAF58255 Olig 29 82.6 3.6 954 22 AAF58252 Olig 29 82.6 3.6 954 22 AAF58252 Olig 20 98.6 5.3 936 22 AAF58252 Olig 20 98.6 5.3 0.5 0.	cDNA encoding muri	AA261736	21	962			31	
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12 467.8 20.3 532 21 AAA29060 BOV1 13 422 18.3 1104 21 AAA94050 Huma 14 372.2 16.2 35828 21 AAA29063 Muri 15 193.8 8.4 198 20 AAX40842 Huma 16 193.4 8.4 196 21 AAA05741 Huma 17 100.4 4.4 936 22 AAF58257 Olig 18 100.4 4.4 936 22 AAF58257 Olig 20 100.4 4.4 936 22 AAF58257 Olig 21 100.4 4.4 936 22 AAF58257 Olig 22 100.4 4.4 936 22 AAF58252 Olig 23 98.6 4.3 936 22 AAF58252 Olig 24 98.6 4.3 936 22 AAF58257 Olig 25 98.6 4.3 936 22 AAF58257 Olig 26 98.6 4.3 936 22 AAF58257 Olig 27 98.6 4.3 936 22 AAF58257 Olig 28 98.6 4.3 936 22 AAF58257 Olig 29 98.6 4.3 936 22 AAF58257 Olig 21 00.4 4.4 938 22 AAF58257 Olig 22 98.6 4.3 936 22 AAF58257 Olig 24 98.6 4.3 936 22 AAF58257 Olig 25 98.6 4.3 936 22 AAF58257 Olig 26 98.6 4.3 936 22 AAF58257 Olig 27 98.6 4.3 936 22 AAF58257 Olig 28 98.6 4.3 936 22 AAF58257 Olig 29 98.6 4.3 936 22 AAF58257 Olig 20 98.6 4.3 936 22 AAF58257 Olig 20 98.6 4.3 936 22 AAF58257 Olig 21 98.6 4.3 936 22 AAF58257 Olig 22 Olig 23 98.6 4.3 936 22 AAF58257 Olig 24 98.6 4.3 936 22 AAF58257 Olig 25 98.6 4.3 936 22 AAF58257 Olig 26 98.6 4.3 936 22 AAF58257 Olig 27 98.6 4.3 936 22 AAF58257 Olig	Oligonucleotide D1	AAF58255	22	938		•	28	O
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12 467.8 20.3 532 21 AAA34050 BOV1 13 422 18.3 1104 21 AAA34050 Huma 14 372.2 16.2 35828 21 AAA29063 Muri 15 193.8 8.4 198 20 AAX40842 Huma 16 193.4 8.4 196 21 AAC05741 Huma 17 100.4 4.4 936 22 AAF58254 Olig 20 100.4 4.4 936 22 AAF58259 Olig 21 100.4 4.4 936 22 AAF58250 Olig 22 100.4 4.4 936 22 AAF58250 Olig 23 100.4 4.4 936 22 AAF58250 Olig 24 100.4 4.4 936 22 AAF58250 Olig 25 100.4 4.4 936 22 AAF58250 Olig 26 100.4 4.4 936 22 AAF58250 Olig 27 100.4 4.4 936 22 AAF58250 Olig 28 98.6 4.3 936 22 AAF58250 Olig 29 98.6 4.3 936 22 AAF58250 Olig 25 98.6 4.3 936 22 AAF58250 Olig 25 98.6 4.3 936 22 AAF58250 Olig 26 98.6 4.3 936 22 AAF58250 Olig 27 100.4 4.4 938 22 AAF58250 Olig 28 98.6 4.3 936 22 AAF58250 Olig 29 98.6 4.3 936 22 AAF58250 Olig 25 98.6 4.3 936 22 AAF58250 Olig	Oligonucleotide D2	AAF58259	22	936			26	C
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2 467,8 20,3 53 21 AAAA29060 Bovine TGF-beta 3 422 118.3 1104 21 AAAA94050 Human DAN/Cerbe 4 372.2 16.2 35828 21 AAAA29063 Murine TGF-beta 5 193.8 8.4 198 20 AAX40842 Human secreted 6 193.4 8.4 196 21 AAC05741 Human secreted 7 100.4 4.4 936 22 AAF58252 Oligonucleotide 8 100.4 4.4 936 22 AAF58254 Oligonucleotide 9 100.4 4.4 936 22 AAF58259 Oligonucleotide 0 100.4 4.4 936 22 AAF58259 Oligonucleotide 0 100.0 4.4 936 22 AAF58259 Oligonucleotide		AAF58262	22	936			21	
2 467.8 20.3 532 21 AAA29060 Bovine TGF-beta 3 427 18.3 1104 21 AAA94050 Human DAN/Cerbe 4 372.2 16.2 35828 21 AAA29063 Murine TGF-beta 5 193.8 8.4 198 20 AAX40842 Human secreted 6 193.4 8.4 196 21 AAC05741 Human secreted 7 100.4 4.4 936 22 AAF58252 Oligonucleotide 8 100.4 4.4 936 22 AAF58254 Oligonucleotide 9 100.4 4.4 936 22 AAF58257 Oligonucleotide		AAF58259	22	936			20	
2 467,8 20.3 532 21 AAA39060 3 422 18.3 1104 21 AAA394050 4 372.2 16.2 38928 21 AAA394050 5 193.8 8.4 198 20 AAX40842 6 193.4 4.4 936 21 AAC95741 7 100.4 4.4 936 22 AAF58252 8 100.4 4.4 936 22 AAF58254 6 190.4 4.4 936 22 AAF58254		AAF58257	22	936	٠		19	
2 467,8 20,3 532 21 AAAA29060 Bovine TGF-beta 3 422 118.3 1104 21 AAAA94050 Human DAN/Cerbe 4 372.2 16.2 35928 21 AAAA29063 Murine TGF-beta 5 193.8 8.4 198 20 AAX40842 Human secreted 6 193.4 8.4 196 21 AAC95741 Human secreted 7 100.4 4.4 936 22 AAF58252 Oligonucleotide	D	AAF58254	22	936	•		18	
2 467.8 20.3 532 21 AAA29060 3 422 18.3 1104 21 AAA94050 4 372.2 16.2 35828 21 AAA29063 Murine TGF-beta 5 193.8 8.4 198 20 AAX40842 6 193.4 8.4 196 21 AAC05741 Human secreted 6 193.4 8.4 196 21 AAC05741 Human secreted	m .	AAF58252	22	936	•		17	
2 467.8 20.3 532 21 AAA29060 Bovine TGF-beta 4 21 18.3 11.04 21 AAA94050 Human DAN/Cerbe 4 372.2 16.2 35828 21 AAA29063 Murine TGF-beta 5 193.8 8.4 198 20 AAX40842 Human secreted		AAC05741	21	196	٠	Ü.	16	
2 467.8 20.3 532 21 AAA29060 Bovine TGF-beta b 3 422 18.3 1104 21 AAA94050 Human DAN/Cerberu 4 372.2 16.2 35828 21 AAA29063 Murine TGF-beta b	secreted	AAX40842	20	198	٠	w.	15	
2 467.8 20.3 532 21 AAA29060 Bovine TGF-beta b 3 422 18.3 1104 21 AAA94050 Human DAN/Cerberu	TGF-beta b	AAA29063	21	10	6.	₽.	14	
2 467.8 20.3 532 21 AAA29060 Bovine TGF-beta b	DAN/Cerberu	105	21		8	N	13	
	TGF-beta b	906	21	532	0	67.	12	

ALIGNMENTS

RESULF AAA29055 ID AAA2 XX AAA2 AC AAA2 XX 12-S XX 12-S XX OSTE KW OSTE KW OSTE KW DONE OS HOMC XX WO2(XX WO2(XX WO2(PN WO2(XX QB-(XX YA) PFT 24-1 XX QB-(XX YA) PFT 27-1 XX YA) osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; chromosome 17q12-21; gene therapy; antisense therapy; fracture; bone mineralization; ss. 27-NOV-1998; 24-NOV-1999; 08-JUN-2000. Homo Human TGF-beta binding protein (BEER) cDNA. AAA29055; AAA29055 standard; cDNA; 2301 BP WO200032773-A1. 12-SEP-2000 ـــ sapiens. (first entry) 98US-0110283 99WO-US27990. Location/Qualifiers 48..689 /*tag= a /product= TGF-beta_binding_protein

Brunkow ME, Van Ness J,

Galas DJ, Kovacevich B, Mulligan JT, Paeper BW; Winkler DG;

(DARW-) DARWIN DISCOVERY LTD

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This cDNA encodes a human transforming growth factor-beta (TGF-beta) binding protein designated BEER. The hBEER gene has been localized to the chromosome 17q12-21. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or
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RESULT 1 US-09-188-930-40 Sequence 40, A Patent No. 615 GENERAL INFORM APPLICANT: Wa APPLICANT: S1 APPLICANT: On APPLICANT: ON TITLE OF INVE TITLE OF INVE TITLE OF INVE FILE REFERENC CURRENT APPLI CURRENT FILLM COURTENT FILLM C		C 4 4	43	4.4	4		ი ი ა		ن د	ıω		c 3				
SULT 1 -09-188-930-40 Sequence 40, Application US/0918 Patent No. 6150502 GENERAL INFORMATION APPLICANT: Watson, James D. APPLICANT: Steeman, Matthew APPLICANT: OF INVENTION: Composition TITLE OF INVENTION: and Methods FILE REFERENCE 11000.1011c1 CURRENT FILING DATE: 1998-11-09 NUMBER OF SEO LD NOS: 348 SOFTWARE: FastSEQ for Windows V		410	.ω.	3 ⊢	0	9	ω.	70	n U	1 A	. ω	N	₽	0	φ	00
SULT 1 -09-188-930-40 Sequence 40, Application US/09188930A Patent No. 6130502 GENERAL INFORMATION: APPLICANT: Watson, James D. APPLICANT: Sleeman, Matthew APPLICANT: Onrust, Rene APPLICANT: MUNISON, James Greg TITLE OF INVENTION: Compositions Isolated TITLE OF INVENTION: and Methods For Their FILE REFERENCE: 11000.1011c1 TITLE OF INVENTION NUMBER. 15/00/108 0300		42.		4 2	Ñ			2.4		ω.						
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Applicat Applicat 150502 RRMATION: Watson, J Strachan, Sleeman, Onrust, R Murison,		<u></u>	1	ب د	<u>, </u>	۳.	<u></u>	H	ے د		<u>, _</u>	<u>-</u>	<u>-</u>	<u>_</u>	<u>.</u>	1.
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40 150502 RMATION: Watson, James D. Strachan, Lorna Strachan, Lorna Strachan, Matthew Onrust, Rene Onrust, Rene Onrust, Rene		20235 5173	20235	1269	835	38506	36778	11847	2634	1578	35935	35935	593	·w	593	593
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CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 209
LENGTH: 962
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
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Local Similarity 52.5%;
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Pred. No. 1.3e-11;
0; Mismatches 239; Indels 2
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                                                                                                                                                                 Query Match
Best Local Similarity
Matches 239; Conserv
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WULLING, J.G:
REGISTRATION NUMBER: 33,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: LIN
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
3.5 INCH DISKETTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: I FILING DATE: 6 June CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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STREET: NOSELAND
CITY: ROSELAND
TRATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: 201-994-1700
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LENGTH: 900 BASE PAIRS
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OPERATING SYSTEM:
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Pred. No. 2.5e-08;
0; Mismatches 224;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



Copyright (c) 1993 - 2000 OM nucleic - nucleic search, using sw model Run on: November 8, 2001, 23:50:4	
Copyright (c) 19 nucleic search, using November 8, 2001	
Copyright (c) 1993 - 2000 Compugen Ltd. Leic search, using sw model November 8, 2001, 23:50:42; Search time 438.73 Seconds (without alignments) 3293.145 Million cell updates/sec	Conform version 4 5

Title: Perfect score: US-09-668-021-5 2301

Scoring table:

Sequence: 1 agagcctgtgctactggaag.....caatgaatcatgaccgaaag 2301

730101 segs, 313950809 residues

Gapop 10.0 , Gapext 1.0

IDENTITY_NUC

Total number of hits satisfying chosen parameters:

1460202

Minimum DB Maximum DB seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database N_Geneseq_0601:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
	2301	100.0	2301	21	AAA29056	Human TGF-beta bin
2	2299.4	99.9	2301	21	AAA29062	Human TGF-beta bin
ω	2297.8	99.9	2301	21	AAA29055	Human TGF-beta bin
4	2296.2	99.8	2301	21	AAA29061	Mutant human TGF-b
5	2277.4	99.0	2329	22	AAA91023	Human secreted pro
6	2047.8	89.0	5680	21	AAA94049	Human DAN/Cerberus
7	2047.8	89.0	9301	21	AAA29064	Human TGF-beta bin
8	638.8	27.8	642	21	AAA94051	Human DAN/Cerberus
9	610	26.5	642	21	AAA29057	Vervet TGF-beta bi
10	533	23.2	674	21	AAA29059	Rat TGF-beta bindi
11	502	21.8	638	21	AAA29058	Murine TGF-beta bi

Brunkow ME, Van Ness J,

Galas DJ, Winkler DG;

Kovacevich B,

Mulligan JT,

Paeper BW;

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Oligonucleotide D1 SA8 virus gB glyco				Human adenosine A1	Homo sapiens fetal	Human adult retina	DNA encoding human	cDNA sequence of h	Human small CCN-li	cDNA encoding smal	Skin cell cDNA, SE	Skin cell cDNA, SE	cDNA encoding muri	cDNA encoding muri	Skin cell cDNA, SE				Oligonucleotide D1						Oligonucleotide D1	Oligonucleotide D1	Oligonucleotide D1		Human secreted pro	Murine TGF-beta bi	Human DAN/Cerberus	Bovine TGF-beta bi

ALIGNMENTS

AAA29056 RESULT osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; variant; V101; gene therapy; antisense therapy; fracture; chromosome 17q12-21; bone mineralization; ss. AAA29056; Human TGF-beta binding protein (BEER) variant V10I cDNA 12-SEP-2000 AAA29056 standard; cDNA; 2301 (DARW-) DARWIN DISCOVERY LTD 24-NOV-1999; 08-JUN-2000. Homo sapiens. 27-NOV-1998; ;;O200032773-A1. (first entry) 98US-0110283. 99WO-US27990. Location/Qualifiers 48..689 /*tag= a /label= BEER_variant_V10I /product= TGF-beta_binding_protein ВP

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Sequence 40, Appl
Sequence 209, App
Sequence 1, Appli
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Sequence 1, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 10, Appli
Sequence 11, Appli
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US-09-188-930-40
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Best Local Similarity
Matches 262; Conserv
                                367
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                                                                        tgcgcgggcgagtgcttgcccctgccggtgcttcccaactggatcggaggaggctacgga 403
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Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Patent No. 5215881	Sequence 4, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	`	Sequence 2, Appli					

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 40
LENGTH: 962
TYPE: DNA
ORGANISM: mouse
US-09-188-930-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40, Application US/09188930A Patent No. 6150502 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                  76 tggcaggccttcaagaatgatgccacggaaatcatccccgagctcggagagtaccccgag 135
ttcacccgctacgtgaccgatgggccgtgccgcaggcccaagccagtcaccgagttggtg
                                                                ttcagtagcactggactggatcgaacagtcgagttcaagtgggctgcagggaactgcgg
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                                                                                            ccccaccaccc---ctttgagaccaaagacgtgtccgagtacagctgccgagagctgcac
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54.7%;
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Gaps

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312

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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: MURISON, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-188-930-209
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RESULT
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GENERAL INFORMATION:
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Best Local
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LENGTH: 962
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54.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 3256
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 900 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: (FILING DATE: 6 June CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hastings, Gregg A. and Adams, Mark D. TITLE OF INVENTION: Human CCN-Like Growth Factor NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: LI
MOLECULE TYPE:
                                                                                                                    413
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                                         473 GAACAAAGTACTGGAGCAGGAGGAGCTCCCAGGAGTGGCGGTGTGTCAATGACAAAACCC
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD CITY: ROSELAND STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.18;
Local Similarity 53.08;
nes 255; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 ggtggcaggccttcaagaatgatgccacggaaatcatccccgagctcggagagtaccccg 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                              GTTCCACCAAATACATCTCTGATGGCCAGTGCACCAGCATCAGCCCTCTGAAGGAGCTGG
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TGTGTGCTGGCGAGTGCTTGCCCCTGCCAGTGCTCCCTAACTGGATTGGAGGAGGCTATG 472
                                                                                                                                                                                                                                                                            ATTTCAGTAACACTGGACTGGATCGGAACACTCGGGTTCAAGTGGGTTGCCGGGAACTGC
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6 June 1995
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /SIDS1/gcgdata
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638
SIDSI/gcgdata/geneseq/geneseqn/Na1980.DAT:

SIDSI/gcgdata/geneseq/geneseqn/Na1981.DAT:

SIDSI/gcgdata/geneseq/geneseqn/Na1982.DAT:

SIDSI/gcgdata/geneseq/geneseqn/Na1983.DAT:

SIDSI/gcgdata/geneseq/geneseqn/Na1983.DAT:

SIDSI/gcgdata/geneseq/geneseqn/Na1984.DAT:

SIDSI/gcgdata/geneseq/geneseqn/Na1985.DAT:

SIDSI/gcgdata/geneseq/geneseqn/Na1986.DAT:

SIDSI/gcgdata/geneseq/geneseqn/Na1987.DAT:

SIDSI/gcgdata/geneseq/geneseqn/Na1989.DAT:

SIDSI/gcgdata/geneseq/geneseqn/Na1999.DAT:

SIDSI/gcgdata/geneseq/geneseqn/Na1999.DAT:

SIDSI/gcgdata/geneseq/geneseqn/Na1992.DAT:

SIDSI/gcgdata/geneseq/geneseqn/Na1993.DAT:

SIDSI/gcgdata/geneseq/geneseqn/Na1993.DAT:
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11	10	9	8	7	0	5	4	w	2		Result
414.2	427	500	500.4	500.4	502	502	502	503.2	556	638	Score
64.9	66.9	78.4	78.4	78.4	78.7	78.7	78.7	78.9	87.1	100.0	Query Match
532	35828	642	2301	2301	2329	2301	2301	642	674	638	% Query Match Length DB
21	21	21	21	21	22	21	21	21	21	21	DB
AAA29060	AAA29063	AAA94051	AAA29062	AAA29061	AAA91023	AAA29056	AAA29055	AAA29057	AAA29059	AAA29058	ID
Bovine TGF-beta bi	Murine TGF-beta bi	Human DAN/Cerberus	Human TGF-beta bin	Mutant human TGF-b	Human secreted pro	Human TGF-beta bin	Human TGF-beta bin	Vervet TGF-beta bi	Rat TGF-beta bindi	Murine TGF-beta bi	Description

WPI; 2000-412321/35

Brunkow ME, Van Ness J,

Galas DJ, Winkler DG;

Kovacevich B,

Mulligan JT,

Paeper BW;

(DARW-) DARWIN DISCOVERY LTD

24-NOV-1999; 08-JUN-2000.

27-NOV-1998;

98US-0110283. 99WO-US27990

			a	C				C	C	C	O	C			C			O	C														
45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
2	42.8	43	43	43	43.2	43.8	44.2	44.4	44.4	46.2	46.2	46.4	47.2	47.2	47.8	52.4	57	65.6	65.6	67.2	67.2	67.2	67.2	83.2	83.2	83.2	83.2	83.2	106	106	Ln.	367.4	367.4
6.7	6.7	. 7	6.7	•	6.8	6.9	6.9	7.0	7.0	7.2	7.2	7.3	7.4	7.4	7.5	8.2	8.9	10.3	10.3	10.5	10.5	10.5	10.5	13.0	13.0	13.0	13.0	13.0	16.6	9	9	57.6	57.6
36778	11220	114955	4020	2075	58857	1388	3930	8091	5617	2007	2007	114955	44377	44377	37856	71989	412	1710	1692	1774	1719	900	900	962	962	962	962	954	198	196	1104	9301	5680
21	21	20	18	18	21	22	21	19	19	20	19	20	18	18	21	21	22	20	21	20	21	19	18	22	22	21	21	22	20	21	21	21	21
AAZ87318	AAZ87298	AAX53491	AAT91361	AAT75444	AAA58471	AAF28262	AAZ44744	AAV57001	AAV57163	AAZ30905	AAV71089	AAX53491	AAT80414	AAT78508	AAA11992	AAA29349	AAF66218	AAX84238	AAC79467	AAX07571	AAA40498	AAV37735	AAT47661	AAC99669	AAC99578	AAZ61736	AAZ61645	AAC99782	AAX40842	AAC05741	AAA94050	AAA29064	AAA94049
S. venezuelae pik	S. venezuelae macr	Human adenosine Al	Orf virus genomic	cDNA encoding oste	Nucleotide sequenc	Monkey MANGO 245 D	Human KLIMP cDNA.	Human Notch3 cDNA.	Partial human Notc	Thermus thermophil	dnaX gene of Therm	Human adenosine Al	Platenolide syntha	Platenolide syntha	S. cellulosum DNA	Sorangium cellulos	Novel human polynu	DNA encoding human		ທ		\neg			cell cDN		cDNA encoding muri	cell cDNA	secreted	Human secreted pro			Human DAN/Cerberus

ALIGNMENTS

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RESULT
AAA29058
CDS
                                                                                                WO200032773-A1.
                                                                                                                                                    Mus musculus.
                                                                                                                                                                osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization; ss.
                                                                                                                                                                                        Murine TGF-beta binding protein (BEER) cDNA.
                                                                                                                                                                                                        12-SEP-2000 (first entry)
                                                                                                                                                                                                                        AAA29058;
                                                                                                                                                                                                                                       AAA29058 standard; cDNA; 638 BP
                                                                                                                                                                                                                                                     /*tag= a
/product= TGF-beta_binding_protein
                                                                                                                                   Location/Qualifiers
                                                                                                                      /*tag=
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Length

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This cDNA encodes a murine transforming growth factor-beta (TGF-beta) binding protein designated mBEER. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with the conservation of treatment and diagnosis of diseases associated with the conservation of disorders associated with decreased TGF-beta BP expression. The cDNA or vectors may be administered to treat diseases by rectifying mutations or conservation in a patient's genome that affect the activity of BEER by conservation of BEER polypeptides. The nucleic acids may be used for recombinant correction of BEER polypeptides. The nucleic acids may be used for recombinant constitution of BEER appears and for identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such as osteopenia, osteoporosis, fractures and other disorders associated with low mineral content.
     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteoporosis and fractures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids (I)
protein, useful f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAY96432
638 BP; 114 A; 224 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding a transforming growth factor beta binding
for identifying agents for treating osteopenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    162pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
     209
  G;
91 T; 0 other;
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밁 ş В Ş 밁 Š Db δÃ Q Q õ Db 밁 밁 В Ş В Ş 망 Š Query Match Best Local Similarity Matches 638; 541 601 541 481 481 421 421 361 361 301 301 241 241 181 181 121 121 61 61 ш aaagccaaccaggcggagctggagaacgcctactagag 999ccggagaccgcgcgccgcagaagggtcgcaagccgcggcccggcgcccggggagcc gcctcgtgcaagtgcaagcgcctcacccgcttccacaaccagtcggagctcaaggaacttc aagtggtggcgcccgaacggaccggatttccgctgcatcccggatcgctaccgcgcgcag aagtggtggcgccgaacggaccggatttccgctgcatcccggattgctaccgcgcgcag ttggtgtgctccggccagtgcggccccgcggggctgctgcccaacgccatcgggcgcgtg ttggtgtgctccggccagtgcggccccgcgcggctgctccaacgccatcgggcgcgtg ctgcactacacccgcttcctgacagacggcccatgccgcagcgccaagccggtcaccgag ctgcactacacccgcttcctgacagacggcccatgccgcagcgccaagccggtcaccgag ggcagacctccccaccatccctatgacgccaaaggtgtgtccgagtacagctgccgcgag ggcagacctccccaccatccctatgacgccaaaggtgtgtccgagtacagctgccgcgag ggagagtaccccgagcctcctcctgagaaccaaccagaccatgaaccgggcggagaatgga glggagggccaggggtggcaagccttcaggaatgatgccacagaggtcatcccagggctt gtggagggccaggggtggcaagccttcaggaatgatgccacagaggtcatcccagggctt 120 atgcagccctcactagccccgtgcctcatctgcctacttgtgcacgctgccttctgtgct atgcagccctcactagccccgtgcctcatctgcctacttgtgcacgctgccttctgtgct gcctcgtgcaagtgcaagcgcctcacccgcttccacaaccagtcggagctcaaggacttc c999t9cagct9ct9tgcccc99gggcgcggcgccgcgctcgcgcaaggtgcgtctggtg ggagagtaccccgagcctcctcctgagaacaaccagaccatgaaccgggcggagaatgga Conservative 100.0%; 0, Score 638; DB 21; Pred. No. 1.4e-124; Mismatches 0; Indels 0; 180 480 480 420 420 300 300 240 180 120 60 540 360 360 240 0;

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밁
24-NOV-1999;
                                                                                                                                                               Rattus norvegicus.
                                                                                                                                                                                                                                                                                                 AAA29059;
                                                                                                                                                                                                                                                                                                                              AAA29059 standard;
                                                          WO200032773-A1
                                                                                                                                                                                                                                        Rat TGF-beta
                                                                                                                                                                                                                                                                     12-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                        601
                                                                                                                                                                                                                                                                                                                                                                                                   aaagccaaccaggcggagctggagaacgcctactagag
                                                                                                                                                                                          gene
                                                                                                                                                                                       c; cransforming growth factor-beta; TGF-beta; binding protein;
therapy; antisense therapy; fracture; bone mineralization; ss
                                                                                                                                                                                                                                     binding
                                                                                                                                                                                                                                                                     (first
 99WO-US27990
                                                                                                                  Location/Qualifiers 33..674
                                                                                     /product= TGF-beta_binding_protein
                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                              CDNA;
                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                               674
                                                                                                                                                                                                                                       (BEER)
                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                        CDNA
                                                                                                                                                                                                                                                                                                                                                                                                       638
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88

RESULT AAA29059 ID AAA29059 ID AAA29059 ID AAA2
XX AAA2 AC AAA2
XX 12-S
XX 12-S
XX OSTE
CO RAT
XX OSTE
KW BEEF
XX WO2(
XX WO2(
PN WPI)
DR P-PE
XX WPI
DR P-PE
X This cDNA encodes a rat transforming growth factor-beta (TGF-beta) binding protein designated rBEER. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patients own production of BEER, polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for alignostic assays and for functional studies. BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such as osteopenia, osteoporosis, fractures and other disorders Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures Sequence disorders such a associated with Brunkow ME, Van Ness J, 27-NOV-1998; (DARW-) 2000-412321/35.)B; AAY96433. DARWIN DISCOVERY LTD 674 Page 125; BP; 128 Galas DJ, Winkler 98US-0110283 low mineral 162pp; English A; 240 βG; Kovacevich B, c; content. 208 ç; 98 Mulligan JT, T; 0 other; Paeper BW;

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δõ
                               Вb
                                                                                    Query Match
Best Local S
Matches 596
   61
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                            atgcagctctcactagcccttgccttgcctgcctgcttgtacatgcagccttcgttgct
                                          atgcagccctcactagccccgtgcctcatctgcctacttgtgcacgctgccttctgtgct
gtggagggccaggggtggcaagccttcaggaatgatgccacagaggtcatcccagggctt 120
                                                                                      11 Similarity 92.8
596; Conservative
                                                                                                  87.1%;
92.8%;
                                                                                   Score 556; DB 21;
Pred. No. 1.7e-107;
0; Mismatches 40;
                                                                                                               Length 674;
                                                                                      Indels
                                                                                      6
                                                                                      Gaps
                               92
                                                         60
                                                                                      1;
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Run

on:

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Title:
Perfect score:
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Maximum Match
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match Length
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   US-09-668-021-11
638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/Packfiles1.seq:*
                  Match 100%
first 45 summaries
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US-09-188-930-40
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US-08-468-8478-1
US-09-443-501A-2
US-08-804-198-1
US-09-162-373-2
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Compugen
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LENGTH: 962
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                                                      353
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Result

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45	44	43	42	41	40	39	38	37	36	3 5	34	ω	32	31	30	29	28
37.2	37.2	37.4	37.8	37.8	37.8	37.8	38	38	38.2	38.2	38.8	39	39	39.4	39.4	40	40
5.8	5. 8	5.9	5.9	5.9	5.9	5.9	6.0	6.0	6.0	6.0	6.1	6.1	6.1	6.2	6.2	6. 3	6.3
4403	4403	1154	2126	2126	2126	2126	16075	16075	11219	11219	33529	1578	675	1780	1780	2943	801
2	ν	4	w	w	w	N	ω	w	w	⊷	4	-	4	ω	N	Н	4
US-08-447-642-1	US-08-284-941-1	US-09-347-803-15	US-09-232-857-1	US-09-058-725B-1	US-09-110-937-1	US-08-789-354-1	US-09-096-867-1	us-09-096-942-1	US-08-439-009A-1	US-07-642-734C-1	US-09-144-085-3	US-08-681-129-1	US-08-998-416-1096	US-08-960-507-5	US-08-933-821-5	US-08-042-747A-7	US-08-757-669A-16
Sequence 1, Appli	Sequence 1, Appli	Sequence 15, Appl	Sequence 1, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 1096, Ap	Sequence 5, Appli	Sequence 5, Appli	 Sequence 7, Appli 	Sequence 16, Appl							

ALIGNMENTS

Minimum Maximum

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; TYPE: DNA
; ORGANISM: mouse
US-09-188-930-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 40, Application Patent No. 6150502 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Occust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 348 SOFTWARE: FastSEQ for Windows Version 3.0
cctcctgagaaccagaccatgaaccgggcggagaatggaggcagacctccc---cac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gccttcaggaatgatgccacagaggtcatcccagggcttggagagtaccc---cgagcct 138
                                                                      gagtgcttgcccctgccggtgcttcccaactggatcggaggaggctacggaacaaagtac
                                                                                                cagtgcggccccgcgcggctgctgcccaacgccatcgggcgcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 83.2; DB 3;
Pred. No. 1.2e-10;
0; Mismatches 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 962;
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US-09-188-930-209
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US-09-188-930-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Compositions Isolated From Skin TITLE OF INVENTION: and Methods For Their Use FILE REFERENCE: 11000.1011c1 CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09 NUMBER OF SEQ ID NOS: 348 SOFTWARE: PastSEQ for Windows Version 3.0 SEQ ID NO 209 LENGTH: 962 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Watson, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 209,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Steachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
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tcqtgcaagtgcaagcgcctcacccgcttccacaaccagtcggagctcaaggacttcggg
                                                         atccagctgcagtgtcaggacggc---agcacgcgcacctacaaaatcaccgtggtcacg
                                                                                  cagtgcggccccgcgggctgctgcccaacgccatcgggcgcg-----tgaag
                                                                                                                                                                                                                                                                                                                          ttcctgacagacggcccatgccgcagcgcccaagccggtcaccgagttggtgttcccggc
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                                                                                                                                                                                                                     gagtgcttgcccctgccggtgcttcccaactggatcggaggaggctacggaacaaagtac 412
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                                                                                                                                        tggagccggaggagctctcaggagtggcggtgtgtcaacgacaagacgcgcacccagagg
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52.8%;
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Pred. No. 1.2e-10;
0; Mismatches 233;
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; Patent No. 5780263
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                       Query Match 10.5%;
Best Local Similarity 50.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US
FILING DATE: 6 June 19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                  364
                                                                                                304
                                                                                                                                                                                                                             184
316 cagtgcggccccgcgggctgctgcccaacgccatcgggcgcgt-----
                                                                                                                                                               244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               590 gtgtcgccagccaagcccgcccagcaccacagagagcggaagagagccagcaaatcca
                                                                                                                                                                                                                                             82 gccttcaggaatgatgccacagaggtcatcccagggcttggagagtaccccgagć---ct 138
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 900 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                              TACATCTCTGATGGCCAGTGCACCAGCATCAGCCCTCTGAAGGAGCTGGTGTGTGCTGGC
                                                   ACTGGACTGGATCGGAACACTCGGGTTCAAGTGGGGTTGCCGGGAACTGCGTTCCACCAAA
                                                                                                                 catccctatgacgccaaaggtgtgtccgagttacagctgccgcgagctgcactacacccgc
                                                                                                                                                             GCTTTTAAAAATGATGCCACAGAAATCCTTTATTCACATGTGGTTAAACCTGTTCCAGCA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccggagaccgcgcgccgcagaagggtcgcaagccggggcccgggggcccggggagcca 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EE: CARELLA, BYRNE, BAIN, SE: CECCHI, STEWART & OLST 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hastings,
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      LINEAR
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N: 435
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Pred. No. 4.9e-07;
0; Mismatches 243;
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                           Result
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length:
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1. /SIDSI/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseqn/NA1984.DAT:*
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674
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                               : /SIDS1/gcgdata/genesed/yeneseqn/Na198.DAT: *
:/SIDS1/gcgdata/genesed/geneseqn/Na198.DAT: *
:/SIDS1/gcgdata/genesed/geneseqn/Na198.DAT: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search time 438.73 Seconds (without alignments) 964.615 Million cell update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Million cell updates/sec
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Human TGF-beta bin
Human TGF-beta bin
Vervet TGF-beta bi
Human DAN/Cerberus
Bovine TGF-beta bi
                                                                                                                                                                                                                     Description
                                                                                                          Human secreted pro
Mutant human TGF-b
                                                                                                                                                               Rat TGF-beta bindi
Murine TGF-beta bi
                                                                                                                                               Human TGF-beta bin
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Platenolide syntha	AAT78508	18	44377	•	45.4	4	
Nucleotide sequenc	AAA58472	21	18660		ज	C 44	_
Recombinant cosmid	AAZ56001	21	38506		46	43	
Nucleotide sequenc	AAA75633	21	38506			42	
. venezuelae	AAZ87285	21	37948		46	41	
S. venezuelae pik	AAZ87318	21	36778			40	
. venez	AAZ87298	21	11220	•	46	39	
=	AAZ30905	20	2007		6,	c 38	_
X gene of	AAV71089	19	2007			ω	_
mays DNA	AAC44071	21	1525		46.6	36	
Rat TGF-beta bindi	AAA29059	21	674		•	c 35	\sim
O	AAV67187	19	1380		4	34	
Signal transductio	AAC84259	22	1125		7.	<u>ω</u>	
Human Notch3 cDNA.	AAV57001	19	8091		49.2	ω	_
Partial human Notc	AAV57163	19	5617		9.	c 31	\sim
S. cellulosum DNA	AAA11992	21	37856		54	w	\sim
Sorangium cellulos	AAA29349	21	71989		4.	29	
Novel human polynu	AAF66218	22	412		56.2	28	
m .	AAX84238	20	1710		ω ·	c 27	_
æ	AAC79467	21	1692		ü	Ν	\sim
S	AAX07571	20	1774		64	25	
	AAA40498	21	1719		64	24	
Human small CCN-li	AAV37735	19	900	9.5	64	23	
encoding sm	AAT47661	18	900		64	22	
cell cDNA,	AAC99669	22	962		2	21	
cell cDN/	AAC99578	22	962			20	
encoding	AAZ61736	21	962		Ν	19	
encoding mur	4	21	962		Ν.	18	
cell cDNA,	AAC99782	22	954		Ν	17	
Human secreted pro	AAX40842	20	198		119	16	
	AAC05741	21	196		119	15	
DAN/Cerbe	AAA94050	21	1104		64.	14	
TGF	906	21	9301		372.6	13	
Human DAN/Cerberus	AAA94049	21	5680		72.		

ALIGNMENTS

osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization; ss

Rat TGF-beta binding protein (BEER) cDNA

12-SEP-2000 AAA29059;

(first entry)

RESULT

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AAA29059 standard; cDNA; 674

ВP

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AAA29059
ID AAA2
XX
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DT 12-S
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FT CDS
FT
WPI; 2000-412321/35
                                                                                  Brunkow ME, Galas DJ,
Van Ness J, Winkler DG;
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                                                                                                                                                                                                                          (DARW-) DARWIN DISCOVERY LTD.
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                                                                                                                                  Kovacevich B,
                                                                                                                              Mulligan JT,
                                                                                                                                  Paeper BW,
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P-PSDB;

AAY96433

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Claim
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osteoporosis and fractures Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia,

English.

disorders associated with decreased TGF-beta BP expression. The cDNA or vectors may be administered to treat diseases by rectifying mutations or deletions in a pattient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patients own production of BEER, polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for diagnostic assays and for functional studies. BEER may be used to raise antibodies and for identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such as osteopenia, osteoporosis, fractures and other disorders associated with low mineral content. This cDNA encodes a rat transforming growth factor-beta (TGF-beta) binding protein designated rBEER. The cDNA and protein may be used fo prevention, treatment and diagnossis of diseases associated with inappropriate BEER expression. For example, they may be used to treat for

Sequence 674 BP; 128 A; 240 C; 208 G; 98 T; 0 other;

21;

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Query Match 82.8
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Matches 596; Conservative

82.5%;

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disorders such as osteopenia, osteoporosis, fractures and other associated with low mineral content.

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                                           This cDNA encodes a murine transforming growth factor-beta (TGF-beta) binding protein designated mBEER. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patients own production of BEER polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for diagnostic assays and for functional studies. BEER may be used to raise antibodies and for identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of
                                                                                                                                                                                                                                Claim 1; Page 123; 162pp; English.
                                                                                                                                                                                                                                                                    Nucleic acids (I) encoding a tra
protein, useful for identifying
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US-08-468-847B-19
US-09-105-537-32
US-09-105-537-32
US-09-105-537-32
US-09-320-878-19
US-08-804-198-1
US-08-804-227C-7
US-08-804-227C-7
US-08-933-221-5
US-09-144-085-3
US-09-158-767-7
US-09-158-767-7
US-09-158-767-7
US-09-158-767-8
US-09-158-767-8
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US-09-158-767-8
US-09-158-767-8
US-09-158-767-1
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Sequence 209, Appli Sequence 2, Appli Sequence 2, Appli Sequence 32, Appli Sequence 19, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 15, Appli Sequence 15, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 6, Appli
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Sequence 209, App
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
38.4	38.4	38.6	38.6	38.6						38.6					39.2	39.4	39.4
5.7	5.7	5.7	5.7	5.7	5.7	5.7				5.7					5.8		
20235	20235	35060	3096	3096	3096	3016	3016	3016	2256	2256	2256	1845	1845	675	459	8854	3624
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US-08-439-009A-3	US-07-642-734C-3	US-08-814-095-7	US-08-814-095-3	US-08-370-156-3	US-08-318-826A-6	US-08-814-095-5	US-08-370-156-5	US-08-318-826A-7	US-08-814-095-1	US-08-370-156-1	US-08-318-826A-5	PCT-US92-06106-1	US-07-732-962A-1	US-08-998-416-1096	US-08-387-942C-9	US-09-053-549-1	US-09-053-549-7
Sequence 3, Appli	Sequence 3, Appli	Sequence 7, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 6, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 7, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1096, Ap	Sequence 9, Appli	Sequence 1, Appli	Sequence 7, Appli

ALIGNMENTS

RESULT 1 US-09-188-930-40

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NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASTSEQ for W
SEQ ID NO 40
LENGTH: 962
TYPE: DNA
ORGANISM: mouse
US-09-188-930-40
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.9
Matches 292; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Watson, James D.
APPLICANY: Strachan, Lorna
APPLICANY: Sleeman, Matthew
APPLICANY: Onrust, Rene
APPLICANY: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09
173
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                                                     gggcgagtgcttgcccctgccggtgcttcccaactggatcggaggaggctacggaacaaa 408
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Pred. No. 1.2e-1
0; Mismatches 2
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227;
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CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 209
LENCTH: 962
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 292; Conserv
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: MURISON, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
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                 458
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gcgggtgcagctgctgttgccccggcgcgcggcgccgcgctctgcgcaaggtgcgtctggt 517
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                                                gtactggagccggaggagctctcaggagtggcggtgtgtcaacgacaagacgcgcaccca 468
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Pred. No. 1.2e-10;
0; Mismatches 227;
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STRANDEDNESS:
TOPOLOGY: LINE
MOLECULE TYPE: CUS-08-468-847B-1
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US-08-468-847B-1
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                                                                                                                                                                            Query Match 9.5%;
Best Local Similarity 48.0%;
Matches 258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: U.
FILING DATE: 6 June 1:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hastings, Gregg A. and Adams, Mark TITLE OF INVENTION: Human CCN-Like Growth Fact
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 900 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                             114 gccttcaagaatgatgccacagaaatcatcccgggactcagagagtacccagagcctcct 173
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OPERATING SYSTEM: WORD PERFECT 5.1
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234 catecttatgaeaceaaagaegtgteegagtaeagetgeegegagetgeactaeaceege
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TYPE: NUCLEIC ACID
TYPE: NUCLEIC SING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: CARELLA, BYRNE, ADDRESSEE: CECCHI, STEWART STREET: 6 BECKER FARM ROAD
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 Mismatches

                                                                                                                                                                                              Score 64; DB 1;
Pred. No. 2.4e-06;
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                                                                                                                                                                               265;
                                                                                                                                                                                                                 Length 900
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd
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Platenolide syntha	Human telomerace r	Homo sapiens mamma	D	DNA encoding a hum	Human alpha-la adr	Alpha-lA adrenergi	Alpha la adrenergi	Lipopolysaccharide	HIV codon-optimize	HIV synthetic Gag	Sorangium cellulos	Sorangium cellulos	Nucleotide sequenc	Human secreted pro	Human secreted pro	Human adenosine Al	Human adenosine Al	S. cellulosum DNA	Novel human polynu	Homo sapiens fetal	Human adult retina	DNA encoding human	cDNA sequence of h	_		cell		cDNA encoding muri	cDNA encoding muri	Skin cell cDNA, SE	Murine TGF-beta bi	Human DAN/Cerberus	

ALIGNMENTS

osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization; ss AAA29060 standard; cDNA; 532 Brunkow ME, Van Ness J, 27-NOV-1998; 24-NOV-1999; 08-JUN-2000. W0200032773-A1 Bos taurus. Bovine TGF-beta binding protein (BEER) cDNA. 12-SEP-2000 (first entry) AAA29060; (DARW-) DARWIN DISCOVERY LTD. H Galas DJ, Winkler DG; 98US-0110283. 99WO-US27990. Location/Qualifiers /partial /product= TGF-beta_binding_protein /*tag= a Kovacevich B, ΒP Mulligan JT, Paeper BW;

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P-PSDB; AAY96434.
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Pred. No. 4.8e-95;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated, human DNA/Cerberus related protein 6 which natural homologue, and polypeptides comprising DCR6 domain acids encoding the proteins which are useful as probes and
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antagonist; BMP; cell growth; cell differentiation; bone formation;
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Pred. No. 1.3e
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Ski
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000,1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08468847B Patent No. 5780263
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hastings, Gregg A. and Adams, Mark D. TITLE OF INVENTION: Human CCN-Like Growth Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: MULLINS, J.G.
 346
                                     491
                                                                                                       431
                                                                                                                                       238
                                                                                                                                                                           371
                                                                                                                                                                                                           178
                                                                                                                                                                                                                                           311
                                                                                                                                                                                                                                                                             118
                                                                                                                                                                                                                                                                                                               191 AAAATGATGCCACAGAAATCCTTTATTCACATGTGGTTAAACCTGTTCCAGCACACCCCA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 6 June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                   1 agaatgatgccacagaaatcatccccgagctgggcgagtaccccgagcctctgccagagc
                                                                                                                         gcccggcgcctgctgcccaacgccatcggccgcggc------aagtggtggc 285
                                                                                                                                                                                           ccgatgggccgtgccgcagcgccaagccggtcaccgagctggtgtgctcgggccagtgcg 237
                                                                                                                                                                                                                                                            ttgagaccaaagacgcctccgagtacagctgccgggagctgcacttcacccgctacgtga 177
                                                                                                                                                                                                                                                                                                                                 tgaacaagaccatgaaccgggcggagaacggagggagacctccccaccc---ct 117
tgttgtgtcctggcgcgcgcgcgcgcgcgcaaggtgcgcctggtggcctcgtgca
                                     GGAGGAGCTCCCAGGAGTGGCGGTGTCTCAATGACAAAACCCCGTACCCAGAGAATCCAGC
                                                                TGCCCCTGCCAGTGCTCCCTAACTGGATTGGAGGAGGCTATGGAACAAAGTACTGGAGCA 490
                                                                                                                                                                                                                                           TGGATCGGAACACTCGGGTTCAAGTGGGTTGCCGGGAACTGCGTTCCACCAAATACATCT
                                                                                                                                                                         242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: CECCHI, STEWART
6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            900 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINEAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 72.2; DB 1;
Pred. No. 4e-07;
0; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 18;
                                                                                                                                                                           430
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

November 7, 2001, 15:46:18; Search time 54.26 Seconds (without alignments)
299.027 Million cell updates/sec

Title: Perfect score: US-09-668-021-2 1167

Sequence: MQLPLALCIVCLLVHTAFRV.....KPRPRARSAKANQAELENAY 213

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

219241 seqs, 76174552 residues

219241

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq seq length: 0 length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : ω 2 I. PIR_68:* pir1:*
pir2:*
pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	Ø	5	4	ω	2	_	No.	Result	
77	77	77.5	78	78	78		78.5	78.5	79	79	79	79	80	81	81	81.5	81.5	82	82.5	83.5	83.5	85	85.5	86.5	87.5	7	94.5	270	Score		
6.6	6.6	6.6	6.7	6.7	6.7	6.7	6.7		6.8			6.8					7.0	7.0	7.1	7.2	7.2	7.3	7.3	7.4	7.5	7.5	8.1	23.1	Match I	Query	P
343	118	1042	1210	1142	877	1122	690	166	866	178	178	118	2333	839	270	969	520	2531	1480	972	824	1469	715	1138	601	158	159	134	Length I		
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G35070	PN0139	A57534	GQHUE	T30272	I50591	T14180	T33321	I51242	T29197	A47291	I51824	PN0141	GNNY2F	I50590	S71793	A70912	S47142	T16743	A36665	T10023	T10020	B36665	T12534	G85077	T22025	A61091	151373	T08710	ID		
apolipoprotein H-r	beta cha	(clone	epidermal growth f	hypothetical prote			hypothetical prote	luteinizing hormon	hypothetical prote	probable finger pr	tumor-suppressive	lutropin beta chai	genome polyprotein	class I INCENP pro		probable leus prot	≫	hypothetical prote	slit protein 1 pre	leucinetRNA liga	inetRNA		hypothetical prote	probable polyprote	hypothetical prote	lutropin beta chai		hypothetical prote			

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
74	74.5	75	75	75.5	75.5	75.5	76	76	76.5	76.5	77	77	77	77	77
6.3	6.4	6.4	6.4	6.5	6. 5	6.5	6.5	6.5	6.6	6.6	6.6	6.6	6.6	6.6	6.6
269	1063	2153	992	1436	646	403	2142	398	1223	402	864	864	702	562	510
2	Ν	2	Ν	Ν	N	N	N	2	N	N	2	N	Ν	Н	2
E69381	T03743	T30074	A31666	A46496	T02398	C70832	в35098	A35281	S29717	T48729	T04518	н85335	E72775	UKHUT	A42750
hypothetical prote		hypothetical prote	hypothetical prote		hypothetical prote	hypothetical prote	MHC class III hist	integumentary muci		hypothetical prote	hypothetical prote	hypothetical prote	probable helicase	t-plasminogen acti	insulinoma-associa

ALIGNMENTS

hypothetical protein DKFZp564D206.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999 C; Accession: T08710

R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, March 1999

A; Reference number: Z16471 A; Accession: T08710

A; Molecule type: mRNA A; Residues: 1-134 <WAM> A; Cross-references: EMBL: AL050024

A; Experimental source: fetal brain; clone DKFZp564D206 C; Genetics:

A; Note: DKFZp564D206.1

Ş Query Match 23.1%; Score 270; DB 2; Best Local Similarity 44.2%; Pred. No. 5.2e-17; Matches 57; Conservative 23; Mismatches 43 80 CRELHFTRYVTDGPCRSAKPVTELVCSGQCGFARLLPNAIGRG---KWW-RPSGPDFRCI 135 43; Length 134; Indels 6, Gaps 4;

DЬ w CRELRSTKYISDGQCTSISPLKELVCAGECLLLPVLPNWIGGGYGTKYWSRRSSQEWRCV 62

136 PDRYRAQRVQLLCPGGEAPRARKVRLVASCKCKRLTRFHNQSELKDFGTEAARPQKGRKP 195

Qy 63 NDKTRTQRIQLQCQDG-STRTYKITVVTACKCKRYTRQHNESSHNFESMSPAKPVQHHRE 121

δÃ 196 RPRA-RSAK 203

В

밁 122 RKRASKSSK 130

N

luteinizing hormone beta subunit - turkey
C;Species: Meleagris gallopavo (common turkey)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: I51373

C;Accession: T51373

R;You, S.; Foster, L.K.; Silsby, J.L.; el Halawani, M.E.; Foster, D.N. J. Mol. Endocrinol. 14, 117-129, 1995

A;Title: Sequence analysis of the turkey LH beta subunit and its regul A;Reference number: I51373; MUID:95290073 its regulation by gonado

A;Reference number: 151373; MUID:95290073
A;Accession: 151373
A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA A; Residues: 1-159 < YOU> A;Cross-references: GB:L35519; NID:g530952; PIDN:AAA74125.1; PID:g530953

C; Genetics:

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C;Genetics:
A;Gene: CESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: pituitary glycoprotein hormone beta chain C;Keywords: glycoprotein; hormone; pituitary F:1-39/Domain: signal sequence #status predicted <SIG>F:48-73,62-96,65-127,77-149,111-139,129-132/Disulfide bonds: #status F:52/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
A61091
Action beta chain precursor -
                                                                                                                                                                                                                                                                              R;Smye,
                                                                                                                                                                                                                                                                                                                  hypothetical protein F40E10.4 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N; Alternate names: luteinizing hormone beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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                                                                           A; Map position: X
                                                                                                                                   A;Cross-references: EMBL:Z69792; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F40E10.4
A;Experimental source: clone F40E10
                                                                                                                                                                       A; Residues: 1-601 <WIL>
                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                        A; Status: preliminary; translated from
                                                                                                                                                                                                                            A; Reference number: A; Accession: T22025
                                                                                                                                                                                                                                                                R;Smye, R.
submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                   C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-158 < NOC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A61091
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Best Local
 Query Match
Best Local ( ilarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
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                                                                                              CESP: F40E10.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKWWRPSG--PDFRCIPDRYRAQRVQLL-CPGGEAPRARKVRLVASCKCKR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGRPPHHPFETKDVSEYSCRELHFTRYYTDGPCRSAKPVTELVCSGQCGPARLLPNAIGR 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  --YRSPLGPPPQSACTYGALRYERWALWGCPIGSDPRV-LLPVALSCRCAR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                                                                                     T22025
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32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.5%;
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29.4%;
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20.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 87.5;
Pred. No. 1;
     Score
Pred.
                                                                                                                                                                                                                                                              February 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                            GB/EMBL/DDBJ
     87.5;
No. 3.
DB
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                                                                                                                                                                                                            hypothetical protein DKFZp434B094.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 02-Sep-2000
C;Accession: T12534
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
                                                                                                                                                                                                                                                                                                       RESULT
T12534
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A;Note: DKFZp434B094.1
C;Superfamily: bromodomain homology
F;113-168/Domain: bromodomain homology <BRO>
                                                                                    A; Molecule type: mRNA
A; Residues: 1-715 <WAM>
A; Cross-references: EMB
                                                                                                                                                           submitted to the Protein S
A; Reference number: Z17524
A; Accession: T12534
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C;Genetics:
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A; Residues: 1-1138 <STO>
A; Cross-references: GB:NC_001268;
                                                   A; Experimental C; Genetics:
                                                                                                                                          A; Status: preliminary
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Best Local Similarity
Matches 53; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                            KCKRLTRFHN-----QSELKDFGTEAA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG-PARLLPNAIGRGKWWR--PSGPDFRCIPDRYRAQRVQLLCPGGEAPRARKVRLVASC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HQIDFVPGASLPNRPAYRTNPVETKEL-EKQVNELMERGHI----CESMSP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                        source: adult testis;
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                                                                                                                                                                                                Sequence Database,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28; Mismatches
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Pred. No. 9.1;
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                                                                        clone DKFZp434B094
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Title:
Perfect score:
Sequence:

OM protein

On:

Scoring

table:

BLOSUM62

ALIGNMENTS

Q9nyy3 Q61477 P45973 P10233 P49303 P80664 Q60401 P54739 Q05613 P18406

herpes simp
f genome po
struthio ca

homo sapien

musculu musculu

streptomyce

mus musculu

Q9r012 P53351

homo sapien rattus norv

aus

tebrata; Euteleostomi;
Meleagrididae; Meleagris

BETA SUBUNIT) (LSH-

and its regulation

BY STIMULATING

BETA

Foster D.N.;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MQLPLALCLVCLLVHTAFRV......KPRPRARSAKANQAELENAY 213
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SLIT_DROME
SAL_HUMAN
SYL_MYCTU
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POLG_FMDV1
NK25_MOUSE
LSHB_PHYCA
DAN_RAT
KLF2_HUMAN
LSHB_COTJA
LNCE_CHTCK
EGFR_HUMAN
LSHB_BALAC
LAL_HUMAN
LSHB_BALAC
LAL_HUMAN
                                                                   TPA, HUMAN
MUBI_XENLA
BAT2_HUMAN
BAT2_HUMAN
HKZ5_RAT
ATH1_HUMAN
WC11_BOVIN
U.SHB_CERS1
EBM6_EBV
LSHB_MACRU
KLF4_HUMAN
KLF4_MOUSE
H15_DROME
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mus musculu
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gallus gall
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   RESULT 1
LSHB_MM
AC P45646
DT 01-NOV
PFIAM; PRO0007; Cys_knot; 1.

PRINTS; PRO0438; GFCYSKNOT.

PROSITE; PS00438; GFCYSKNOT.

PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.

PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.

HORMONE; Signal; Glycoprotein.

SIGNAL 1 39 LUTROPIN BETA
CHAIN 40 159
DISULFID 48 96 BY SIMILARITY
DISULFID 62 111
DISULFID 62 111
DISULFID 65 149 BY SIMILARITY
DISULFID 73 127 BY SIMILARITY
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YOU S., Foster L.K., Silsby J.L., el Halawani M.E., Foster D.N.;

YOU S., Foster L.K., Silsby J.L., el Halawani M.E., Foster D.N.;

"Sequence analysis of the turkey LH beta subunit and its regulat

"Sequence analysis of the turkey LH beta subunit and its regulat

by gonadotrophin-releasing hormone and prolactin in cultured

pituitary cells.";

J. Mol. Endocrinol. 14:117-129(1995).

J. MOI. Endocrinol. 14:117-129(1995).

THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.

-1- SUBUNIT: HETERODINER OF A COMMON ALPHA CHAIN AND A UNIQUE BE

CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,

LUTROPIN, FOLLITROPIN AND GONADOTROPIN.

LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000359; -.
InterPro; IPR001545; -.
InterPro; IPR002400; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L35519; AAA74125.1; HSSP; P01233; 1HRP.
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een the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no resti
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SNK_RAT
SNK_HUMAN
DAN_MOUSE
CBX5_HUMAN
UL49_HSV11
POLG_FMDV2
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Best Local S
Matches 32
                                                   ElyBase: FBgn0010114; hig.
InterPro; IPR000436; -
InterPro; IPR003006; -
Pfam; PF00047; 1g; 1.
Pfam; PF00047; sushi; 5.
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Q09101;
01-NOV-1995
01-NOV-1995
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93213498; PubMed-8461133;
Hoshino M., Matsuzaki F., Nabeshima Y.-I., Hama C.;
"Hikaru genki, a CNS-specific gene identified by abnormal locomotion in Drosophila, encodes a novel type of protein.";
Neuron 10:395-407(1993).
-1- FUNCTION: HAS A ROLE IN THE DEVELOPMENT OF CNS FUNCTIONS INVOLVED IN LOCOMOTOR ACTIVITY.
                                                                                                                                                                                       EMBL; D13884; BAA02984.1; --
EMBL; D13885; BAA02985.1; --
EMBL; D13886; BAA02986.1; --
EMBL; D13887; BAA02987.1; --
EMBL; D13887; BAA02988; BAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
Glycoprotein; Alternative
Sushi; Signal.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
LOCOMOTION-RELATED PROTEIN HIKARU GENKI PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: EXTRACELLULAR.
ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1, 2, 3 (SHOWN HERE) AND RALTERNATIVE PRODUCTS: 5 PLICTING.

PRODUCED BY ALTERNATIVE SPLICTING.

TISSUE SPECIFICITY: EXPRESSED IN PCC NEURONS AND NEUROBLAST IN THE PROCEPHALIC NEUROGENIC REGION IN THE CENTRAL MERVOUS SYSTEM.

SYSTEM.

BEVELOPMENTAL STAGE: MOST ABUNDANT DURING AND/OR AFTER NEUROPPELOPMENTAL STAGE: MOST ABUNDANT DURING CONTAINS.

SIMILARITY: CONTAINS 4 SUSHI (SCR) DOWNAIN.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPLGRP--PQSSCTYGALRYERWALWGCPIGSDPRV-LLPVALSCRCAR 131
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                                  splicing; Immunoglobulin domain; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WW
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N-LINKED (GLCNAC. . .) (P
52B50C8C879653C6 CRC64;
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.065;
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IN THE CENTRAL NERVOUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
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RESULT 3
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Best Local S
Matches 47
                                                                                                                                                                                                                                                                                                       DAN_HUMAN
P41271;
01-FEB-1995
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VARSPLIC
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CHAIN
DOMAIN
                                                      MEDLINE-94366724; PubMed-8084583; Enomoto H., Ozaki T., Takahashi E., Takahashi H., Ohnuma N., Tanabe M., Sakiyama S.;
"Identification of human DAN gene, mapping neuroblastoma tumor suppressor locus."; Oncogene 9:2785-2791(1994).
-i- FUNCTION: POSSIBLE CANDIDATE AS A THMORE
                                                                                                                                                                    AN).

NBLI OR DAN.

HOMO sapiens (Human).

Homo sapiens (Human).

"horia; Metazoa; Chordata;

"horia; Primates;
                                                                                                                                                                                                                                                DAN)
                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
NEUROBLASTOMA SUPPRESSOR OF TUMORIGENICITY 1 (ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
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DOMAIN
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                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                     NCBI_TaxID=9606;
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BY SIMILARITY.
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Pred. No.
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LOCOMOTION-RELATED PROTEIN HIKARU

IG-LIKE C2-TYPE DOMAIN.

SUSHI 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL ATTACHMENT
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                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                         Nomura
Iwai J
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   TUMOR
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                                                                         ı N., Tabata
J., Yoshida
                                              ö
 SUPPRESSOR GENE
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                                              the
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                                                                                          Tabata
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                                              putative
                                                                                                                                                                                                                                                                FINGER PROTEIN
                                                                                                                                                                                                  Euteleostomi;
                                                                         Η.,
                                                                                        s.,
                                                                             Matsunaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LCATNEE
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Q9wx60 acetobacter
Q9y7f8 drosophila
Q9y7f8 drosophila
Q9y7f9 drosophila
Q9y7f9 drosophila
Q9y7f9 drosophila
Q9y7f9 drosophila
Q9y7f9 drosophila
Q91980 caenorhabdi
Q21980 caenorhabdi
Q21980 caenorhabdi
Q7041 xenopus lae
Q9y718 drosophila
Q7041 xenopus lae
Q9y718 homo sapien
Q9y857 homo sapien
Q9y557 homo sapien
Q9y557 homo sapien
Q9y557 homo sapien
Q90101 oryza sativ
Q9d662 trifolium r
Q9nf05 oryza sativ
Q76065 homo sapien
Q9djdl foot-and-mo
Q9djdl foot-and-mo
Q9djdl foot-and-mo
Q9djdl foot-and-mo
Q9ujd7 homo sapien

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of hits satisfying chosen parameters:
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length: 2000000000
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Sp_archea:*

Sp_archea:*

Sp_fungl:*

Sp_fungl:*

Sp_fungan:*

Sp_numan:*

Sp_mammal:*

Sp_mammal:*

Sp_organel1

Sp_organel1

Sp_plant:*

Sp_plant:*

Sp_unclass:

Sp_virus:*

Sp_virus:*
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Match
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Copyright (c) 1993 - 2000 Compugen Ltd
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sp_mhc:*
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sp_phage:*
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sp_vertebrate:*
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Q9MFB6
Q9MFB6
1 Q9JFW7
1 Q35793
1 Q70326
1 Q9Z1K6
3 Q73755
3 Q73755
3 Q9ZPF9
Q9Y4Q3
Q9Y560
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3 Q9PWB0
3 Q9PUK2
Q9H772
Q9UEM9
1 Q88273
060565
Q95376
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O9y3u3 homo sapien
O9pwk0 gallus gall
O9puk2 gallus gall
O9puk2 gallus gall
O9ph772 homo sapien
O88273 mus musculu
O60565 homo sapien
O98276 homo sapien
O99b26 homo sapien
O99b26 homo sapien
O99b26 homo sapien
O99b26 homo sapien
O97b26 mus musculu
O37759 rattus norv
O70326 mus musculu
O37755 gallus gall
O73754 xenopus lae
O9zpf o arabidopsis
O9y4q3 homo sapien
O9v560 drosophila
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Best Local Similarity
Matches 57; Conserv
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Q993U3;
01-NOV-1999 (TrEMBLrel 12, Created)
01-NOV-1999 (TrEMBLrel 12, Last sequence update)
01-MAY-2000 (TrEMBLrel 13, Last annotation update)
HYPOTHETICAL 15.3 KDA PROTEIN (FRAGMENT).
DKFZP564D206.
                                                                                                                                                                                                                                                                                      Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann Submitted (MAY 1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ALOS0024; CAB43243.1; -.
InterPro; IPR000359; -.
PROSITE; PS01225; CTCK_2; 1.
                                                                                                                                                                                                                                                   Hypothetical protein.
NON_TER 1
SEQUENCE 134 AA; 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                          196
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021980
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09V7U8
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09WX23
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09W6C2
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Total number

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Database

Scoring table: Sequence:

Perfect score:

Result No.

Score

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Indels

6 Gaps

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Best Local s
Matches 32
                Rodriguez Esteban C., Capdevila J., Ec
Ortiz A., Izpisua Belmonte J.C.;
"Caronte, a novel cer-like protein, me
embryonic left-right asymmetry.";
Nature 0:0-0(1999)
EMBL: AF179484; AAD55581.1; -.
InterPro; IPR001359; -.
InterPro; IPR001359; -.
ProDom: PD000357; -: 1.
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chorda
Archosauria; Aves; Neogna
Gallus.
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Q9PUK2;
01-MAY-2000
01-MAY-2000
01-MAR-2001
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Q9PWB0;
01-MAY-2000
01-MAY-2000
01-MAR-2001
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Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000359; -. PROSITE; PS01225; CTCK_2; 1. SMART; SM00041; CT; 1. SEQUENCE 272 AA; 31224 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhu L., M
Levin M.;
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EMBL; AF139721; AAD51610.1;
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heart.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99439862; PubMed=10508582; 
Zhu L., Marvin M.J., Gardiner A.,
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32; Conser
PS01225; CTCK_2;
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Neognathae;
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31224 MW;
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; Galliformes; Phasianidae; Phasiani
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; Galliformes; Phasianidae; Phasianinae;
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RESULT
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DT 01
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Matches 32
 Q9UEM9;
01-MAY-2000
01-MAY-2000
01-MAR-2001
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"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO24848, BAB15026.1;
SEQUENCE 168 AA; 19320 MW; D5A4E4E818BE8COE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA: FLJ21195 FIS, CLONE COL
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                                                                                                                                                                                                                                                                                              2 QLPLALCLVCLLVHTAFRVVEGQGWQAFKNDATEIIPELGEYPEPPPELENNKTMNRAEN
                                                                                                                QCRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPPYRKDAKKFWDHFMLRKNSASEEVVLPIKTNEMHQETCRTLPFSQSVAHESCEKV-IV
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                                                                                                                                                                   CN-SFYIPRHV--
                                                                                                                                                                               CGPARLLPNAIGRGKWWRPSGPDER----CIPDRYRAQRVQLLCPGGEAP-RARKVRLVA 163
                                                                                                                                                                                                                                                                      KLSLSLFLVAVLVKVA------EARKNRPA-----GAIPSPYKDGSSN-----N
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                                                                                                                                                                                                                                              GGRPPHHPFETKDVSEYS-------CRELHFTRYVTDGPCRSAKPVTELVCSGQ 108
                                                                                                                                                                                                                                                                                                                       1 Similarity
45; Conserv
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                                                                                                                 157
(TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                    PRELIMINARY;
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31201 MW;
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23.7%;
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                                                                                                                                                                   KKEEESFQSCAFCKPQRVTSVLVELECPGLDPPFRLKKIQKVK
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                                                                                                                                                                                                                                                                                                                       26;
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Pred. No. 0.01
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -FHVPGPDDRLYTFCSKCLPTKFSMKHFDLNCT-SSV
                                                                                                                                                                                                                                                                                                                                   Score 103;
Pred. No. 0
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                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                    493
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Shibahara T.,
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Perfect score:
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1: SIIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: SIIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
5: /SIIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
6: /SIIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*
8: /SIIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*
9: /SIIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*
11: /SIIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /SIIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*
13: /SIIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*
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Listing first 45 s
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/SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length DB	ength 1		ID	Description
,	1167	100.0	213	21	AAB26106	Human DAN/Cerberus
2	1167	100.0	213	21	AAY96429	Human TGF-beta bin
w	1167	100.0	213	22	AAY97589	Human secreted pro
4	1158	99.2	213	21	AAY96436	Human TGF-beta bin
տ	1157	99.1	213	21	AAY96430	Human TGF-beta bin
6	1146	98.2	213	21	AAY96431	Vervet TGF-beta bi
7	1072	91.9	367	21	AAB26105	Human DAN/Cerberus
8	1050	90.0	213	21	AAY96433	Rat TGF-beta bindi
9	1029	88.2	211	21	AAY96432	Murine TGF-beta bi
10	901.5	77.2	176	21	AAY96434	Bovine TGF-beta bi
11	350.5	30.0	206	21	AAY75981	Murine skin cell p

ALIGNMENTS

RESULT AAB26106 Human; DNA/Cerberus-related protein 6; hDCR6; morphogenic protein; antagonist; BMP; cell growth; cell differentiation; bone formation; gene therapy. Human DAN/Cerberus-related protein 6 (hDCR6) (exons 1 and 15-JAN-2001 (first entry) 12-MAR-1999; 02-MAR-2000; 2000WO-US05537 21-SEP-2000. WO200055193-A2 Homo sapiens. AAB26106; AAB26106 standard; Protein; 99US-0124118 213 A

4).

Economides AN; (REGE-) REGENERON PHARM INC

WPI; 2000-638179/61. N-PSDB; AAA94051.

Novel isolated, human DNA/Cerberus related protein 6 which include natural homologue, and polypeptides comprising DCR6 domain and nucleic acids encoding the proteins which are useful as probes and primers -

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ARY96429
ID AAY9
XX AAY9
AC AAY9
XC AAY9
XX 12-S
XX Huma
XX Oste
KW BEEH
  ο<sub>γ</sub>
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence comprises the amino acid sequence encoded by exons 1 and 4 of the human DAN/Cerberus-related protein 6 (hDCR6) coding sequence. The coding sequence was isolated from a human kidnay cDNA library containing exons 1 and 4 of the sequence, HDCR6 is closely related to the DAN and DCR5 proteins, both of which act as antagonists of morphogenic proteins such as BMP. It is possible that the hDCR6 gene and protein can be used as immunogens, modulators of cell function, growth and differentiation, to reduce undesirable bone formation, to identify DCR6 binding agents, in diagnosis, and in gene therapy.
                                                                                                              Brunkow ME,
Van Ness J,
                                                                                                                                                                                                                                                                                                  osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization.
Claim 2; Page 116; 162pp; English
                                   Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia,
                                                                                                                                                                                                    24-NOV-1999;
                         osteoporosis and fractures
                                                                                        YPI:
                                                                                                                                                                                                                            08-JUN-2000
                                                                                                                                                                                                                                                     WO200032773-A1
                                                                                                                                                                                                                                                                                                                                      Human TGF-beta binding
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                                                                                                                                                    (DARW-) DARWIN DISCOVERY LTD
                                                                                                                                                                           27-NOV-1998;
                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                AAY96429 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213;
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Winkler DO
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RESULT
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CD binding protein designated hBEER. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with CD inappropriate BEER expression. For example, they may be used to treat considered to treat the contract of the constance of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Sim
Matches 213;
09-JUN-1999
20-JUL-1999
03-AUG-1999
110-AUG-1999
17-AUG-1999
17-AUG-1999
17-AUG-1999
31-AUG-1999
31-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                               Secreted protein; human; PRO protein; neoplastic cell growth; tumour; proliferation; leukaemia; lymphoid malignancy; inflammatory disorder; angiogenic disorder; immunologic disorder; PRO7476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY97589;
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RESULT 2 US-09-188-930-286 ; Sequence 286, Application US/09188930A ; Patent No. 6150502 ; GENERAL INFORMATION:

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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Oncust, Rene
APPLICANT: Oncust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION UNMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows, Version 3.0
LENGTH: 206
TYPES: DEPT
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; ORGANISM: Mouse
US-09-188-930-286
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Best Local Similarity 40.2
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08468847B Patent No. 5780263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: ISM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                                                                                  APPLICATION NUMBER: US/08/468,847B
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hastings, Gregg A. and Adams, Mark D. TITLE OF INVENTION: Human CCN-Like Growth Factor NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 FESVSPAKPAQHHRERKRASKSSK 202
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CITY: ROSELAND
STATE: NEW JERSEY
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RESULT 4
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TELEPAX: 201-994-1714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5780263
GENERAL INFORMATION:
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                                                                                                            COMPUTER: IBM PS/2

ODERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER:
FILING DATE:
APPLICATION INFORMATION:
ANDEL MULLINS, J.G.

REGISTRATION NUMBER: 33,073
REPERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-94-1700
                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN, ADDRESSEE: CECCHI, STEWART 6 OLSTEIN
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TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
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MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hastings, Gregg A. and Adams, Mark D. TITLE OF INVENTION: Human CCN-Like Growth Factor NUMBER OF SEQUENCES: 20
                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 IGGGYGTKYMSRKSSQEWRCVNDKTRTQRIQLQCQDG-STRTYKITVVTACKCKRYTRQH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 NESSHNFESMSPAKPVQHHRERKRASKSSK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 NOSELKDFGTEAARPQKGRKPRPRA-RSAK 203
                                                                        TELEPHONE: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6 BECKER | CITY: ROSELAND STATE: NEW JERSEY
LENGTH: 206 AMING
TYPE: AMINO ACID
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 GGRPPHHPFETKDVS---EYSCRELHFTRYVTDGPCRSAKPVTELVCSGQCGPARLLPNA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 GGR--HFSNTGLDRNTRVQVGCRELRSTKYISDGQCTSISPLKELVCAGECLPLPVLPNW 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 LPLA----CILMKSCL-----AFKNDATEIL--YSHVVKPVPAHPSSNSTLNQARN 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07068
                                        206 AMINO ACIDS
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6 June 1995
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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length: 2000000000
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Match
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pir2:*
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151373
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T22025
T10020
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S71793
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C; Genetics: A; Note: DKFZp564D206.1

RESULT 1 T08710 hypothetical protein DKFZp554D206 C;Species: Homo sapiens (man) C;Date: 11-Jun-1999 #sequence_rev C;Accession: T08710 R;Wambutt, R.; Heubner, D.; Mewes submitted to the Protein Sequence A;Reference number: 216471 A;Accession: T08710 A;Molecule type: mRNA A;Residues: 1-134 <wanda a;cross-references:="" a;experimental="" brai<="" embl:al050024="" fetal="" source:="" th=""><th></th><th></th><th></th><th></th><th>37 38</th><th>36</th><th>ω ω 1 4 ω</th><th>32</th><th>31</th><th>30</th></wanda>					37 38	36	ω ω 1 4 ω	32	31	30
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l protein DKFZp564D2O6.1 iomo sapiens (man) Jun-1999 #sequence_revis : T08710) the Protein Sequence D number: Z16471 : T08710 : T08710 Type: mRNA 1-134 < WAM> 1-134 < WAM> tal source: fetal brain;		6.50	1 U U	ი. ა.	0.0	6. 6		0.00	6.6	6.7
FZp564D206. (man) Juence_revi D.; Mewes, 1 Sequence 471 L:AL050024 fetal brain		1436 2 613 2		1223 398					80	2142 2
ision 11-Jun-1999 , H.W.; Gassenhube Database, March 1	ALIGNMENTS	1 JC4070 2 A46496 2 T00077		2 S29717 2 A35281						2 в35098
nt) #text_change 13-Aug-1999 xr, J.; Wiemann, S. 999		protein kinase (EC antigen WC1.1 prec gag-like protein -	t-plasminogen acti hypothetical prote	adenylate cyclase integumentary muci	hypothetical prote hypothetical prote	hypothetical prote	probable helicase	mating type A prot	ropin beta	MHC class III hist

luteinizing hormone beta subunit - turkey
C; Species: Meleagris gallopavo (common turkey)
C; Species: Meleagris gallopavo (common turkey)
C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C; Accession: I51373
R; You, S.; Foster, L.K.; Silsby, J.L.; el Halawani, M.E.; Foster, D.N.
J. Mol. Endocrinol. 14, 117-129, 1995
A; Title: Sequence analysis of the turkey LH beta subunit and its regulation
A; Reference number: I51373; MUID:95290073
A; Accession: I51373; MUID:95290073
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-159 < YOU>
A; Construction of the turkey provided from CB/EMBL/DDBJ
A; Construction o C; Genetics: A; Gene: LH-beta Qγ DЬ Qy Вþ Qy Query Match Best Local Similarity Matches 57; Conserv 196 RPRA-RSAK 203 122 RKRASKSSK 130 136 PDRYRAQRVQLLCPGGEAPRARKVRLVASCKCKRLTRFHNQSELKDFGTEAARPQKGRKP 195 63 NDKTRTQRIQLQCQDG-STRTYKITVVTACKCKRYTRQHNESSHNFESMSPAKPVQHHRE 121 80 CRELHFTRYVTDGPCRSAKPVTELVCSGQCGPARLLPNAIGRG---KWW-RPSGPDFRCI 135 3 CRELRSTKYISDGQCTSISPLKELVCAGECLLLPVLPNWIGGGYGTKYWSRRSSQEWRCV 62 Conservative 23.2%; Score 270; DB 2; 44.2%; Pred. No. 3.4e-17; 23; Mismatches 43; subunit and its regulation by Length 134; Indels 6; 4; gonado

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hypothetical protein F40E10.4 - Caenorhabditis elegans (fragment) C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Superfamily: pituitary glycoprotein hormone beta cha C:Keywords: glycoprotein; hormone; pituitary F:1-39/Domain: signal sequence #status predicted <SIG>F:48-73,62-96,65-127,77-149,111-139,129-132/Disulfide; F:52/Binding site: carbohydrate (Asn) (covalent) #statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-158 <NOC>
C; Superfamily: pituitar:
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A;Title: Molecular cloning and nucleotide sequence analysis of A;Reference number: A61091; MUID:89374710
A;Accession: A61091
A;Status: not compared with conceptual translation
                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-601 <WIL>
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                                                                                                                                                 A;Cross-references: EMBL:Z69792; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F40E10.4
                                                                                                                                                                                                                          A; Reference number: A; Accession: T22025
                                                                                                                                                                                                                                                                                 R;Smye,
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Query
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Gallus gallus (chicken)
Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
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 Local Similarity
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                   Mat.ch
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32; Conservative
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 . 5%;
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 Score
Pred.
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87.5;
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R; Eiglmeier, K.; Honore, N.; Woods, S.A.; Mol. Microbiol. 7, 197-206, 1993
Mol. Microbiol of an ordered cosmid library
                                                                                                                                                                                                                                                                                                                                 leucine--tRNA ligase (EC 6.1.1.4) - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change
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A; Accession: T10020
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C;Species: Mycobacterium leprae
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
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                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-972 <EIG>
                                                                                                                                                                                                                                        A; Title: Use of an ordered cosmid library A; Reference number: Z16917; MUID: 93188700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: leucine--tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: Z70722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-824 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Cole, S.T.
submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Cole,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: T10020
                                                                                                                                                         A; Cross-references:
                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBG
                                                                                                                                                                                                                         A; Accession: T10023
                                                                                                                                                                                                                                                                                                              C; Accession:
                                                                                                       Superfamily:
                                                                                                                         Gene:
                                                                                                                                          Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKDVSEYSCRELHFTRYVT---DGPCRSAKPVTELVCSGQCGPARLLPNAIGRGKWWRPS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGHNVLHAMGFDAFGLPAEQYAMQTGTHPRILTEA - - NVVNFRHQLGRLGLGHDSRRTFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAFRVVEGQGWQAFKNDATEIIRELGEYPEPPPELENNKTMNRAENG----GRPPHHPFE
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                                                                                    aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity 38; Conserv
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. Similarity
38; Conserv
                                                                                                                                                                                                                                                                                                                  T10023
                                                                                                       leucine--tRNA ligase
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                                                                                                                                                         EMBL:Y14967; NID:g2370268; PIDN:CAA75192.1; PID:g2370271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -YRAQRVQLLCPG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.3%;
                7.3%;
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Score 84.5; D
Pred. No. 11;
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 84.5; C
Pred. No. 9.1;
15; Mismatches
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                                                                                    ATP; ligase; protein biosynthesis
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                                   DВ
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                                                                                                                                                                                                                                                                                                 B.; Cole,
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                                                                                                                                                                                                                                                                of Mycob
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Matches

Conservative

15;

76;

Indels

17;

Gaps

6;

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Title:
Perfect score:
Sequence:
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB seq
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length: 2000000000
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Match
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93435 segs, 34255486 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-668-021-6
1165
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length DB
            2001, 16:01:12; Search time 31.13 Seconds (without alignments) 234.385 Million cell updates/sec
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       LSHB_MELGA
DAN_HUMAN
SYL_MYCLE
LSHB_TRIVU
SLIT_DROME
SYL_MYCTU
LSHB_DHYCA
DAN_RAT
TONB_PSEP
MCALTUMAN
HX25_HUMAN
BCAL_HUMAN
POLG_FMDV1
LSHB_COTUA
AHG_DROME
EGFR_HUMAN
SFRB_HUMAN
SFRB_HUMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
p41571 homo sapien
Q50192 mycobacteri
Q50192 mycobacteri
Q60192 mycobacteri
Q60198 mycobacteri
Q71198 mycobacteri
Q71198 mycobacteri
Q71191 mus musculu
Q71191 homo sapien
Q71191 homo sapien
Q71191 homo sapien
Q71191 pseudomonas
Q71191 pseudo
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LSHB_MELGA
ID LSHB_MELGA
AC P45646;
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45	44	43	42	41	40	39	38	37	36	35	34
/2	72.5	72.5	72.5	73	73	73	73.5	73.5	73.5	73.5	74
6.2	5.2	6.2	6.2	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.4
3/9	755	375	128	972	191	178	685	682	682	301	2715
-	- ب	μ.	μ	Н		سز	۳	٢	۳	سز	H
CIRO_MOUSE	RRE1_HUMAN	CE10_CHICK	LSHB_STRCA	POLS_IPNVN	CBX5_HUMAN	DAN_MOUSE	SNK_HUMAN	SNK_RAT	SNK_MOUSE	UL49_HSV11	TRX2_HUMAN
P18406 mus musculu		P19336 gallus gall		•		-					Q9umn6 homo sapien

STANDARD;

PRT;

159 AA

	888888888	CCCCCCCTTTTXXXXXX	00000000000000000000000000000000000000
DR HSSP; L35519; AAA74125.1; ALT_INIT. DR HSSP; P01233; 11RP. DR InterPro; IPR001359; DR InterPro; IPR001545; DR InterPro; IPR001545; DR Pfam; PF00007; Cys_knot; 1. DR PRINTS; PR00438; GFCYSKNOT. DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1. DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1. KW HOTMONE; Signal; Glycoprotein. FT SIGNAL 1 1 39 POTENTIAL. FT SIGNAL 40 159 LUTROPIN BETA CHAIN. FT CHAIN 40 159 BY SIMILARITY. FT DISULFID 65 119 BY SIMILARITY. FT DISULFID 65 149 BY SIMILARITY. FT DISULFID 73 127 BY SIMILARITY. FT DISULFID 77 129 BY SIMILARITY.	This SWISS-PROT entry is copyright. It is probetween the Swiss Institute of Bioinformatic the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. I entities requires a license agreement (See ht or send an email to license@isb-sib.ch).	RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RC TISSUB-Pituitary; RX MEDLINE-95290073; pubMed=7772235; RX MEDLINE-95290073; pubMed=7772235; RX YOU S., FOSTER L.K., Silsby J.L., el Halawani M.E., FoSTER D.N.; RA YOU S., FOSTER L.K., Silsby J.L., el Halawani M.E., FoSTER D.N.; RA YOU S., FOSTER L.K., Silsby J.L., el Halawani M.E., FoSTER D.N.; RA YOU S., FOSTER L.K., Silsby J.L., el Halawani M.E., FoSTER D.N.; RA YOU S., FOSTER L.K., Silsby J.L., el Halawani M.E., FoSTER D.N.; RA YOU S., FOSTER L.K., Silsby J.L., el Halawani M.E., FoSTER D.N.; RA YOU S., FOSTER L.K., Silsby J.L., el Halawani M.E., FoSTER D.N.; RA YOU S., FOSTER L.K., Silsby J.L., el Halawani M.E., FoSTER D.N.; RA YOU S., FOSTER L.K., Silsby J.L., el Halawani M.E., FoSTER L.K., RA YOU S., FOSTER L.K., SILSBY J.L., el Halawani M.E., FOSTER L.K., RA YOU S., FOSTER L.K., SILSBY J.L., el Halawani M.E., FOSTER L.K., RA YOU S., FOSTER L.K., SILSBY J.L., el Halawani M.E., FOSTER D.N.; RA YOU S., FOSTER L.K., SILSBY J.L., el Halawani M.E., FOSTER D.N.; RA YOU S., FOSTER L.K., SILSBY J.L., el Halawani M.E., FOSTER D.N.; RA YOU S., FOSTER L.K., SILSBY J.L., el Halawani M.E., FOSTER D.N.; RA YOU S., FOSTER L.K., SILSBY J.L., el Halawani M.E., FOSTER D.N.; RA YOU S., FOSTER L.K., SILSBY J.L., el Halawani M.E., FOSTER D.N.; RA YOU S., FOSTER L.K., SILSBY J.L., el Halawani M.E., FOSTER D.N.; RA YOU S., FOSTER L.K., SILSBY J.L., el Halawani M.E., FOSTER D.N.; RA YOU S., FOSTER L.K., SILSBY J.L., el Halawani M.E., FOSTER D.N.; RA YOU S., FOSTER L.K., SILSBY J.L.; RA YOU S., FOSTER L.K., SILSBY J.L., el Halawani M.E., FOSTER L.K., el Halawani M.E., el Halawani M.E., FOSTER L.K., el Halawani M.E., FOSTER L	
·	duced through a collaboration s and the EMBL outstation are no restrictions on its its content is in no way Usage by and for commercial tp://www.isb-sib.ch/announce/	and its regulation in cultured fron By STIMULATING ND A UNIQUE BETA OTHYROTROPIN,	WE BETA SUBUNIT) (LSH- a; Euteleostomi; grididae; Meleagris.

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RESULT 2
DAN_HUMAN
ID DAN_H
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Matches 33
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Best Local S
Matches 32
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P41271;
01-FEB-1995 (
01-FEB-1995 (
01-OCT-2000 (
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                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                neuroblastoma tumor suppressor Oncogene 9:2785-2791(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94366724; PubMed-8084583;
Enomoto H., Ozaki T., Takahashi E.,
Takahashi H., Ohnuma N., Tanabe M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enomoto H., Ozaki T., Takahashi H., Ohnuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                         SEQUENCE
                                                                                                                                                                          EMBL; D28124; BAA05671.1;
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                                                                                                                                   ZN_FING
                                                                                                                                               Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of human DAN gene, mapping neuroblastoma tumor suppressor locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakiyama S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                       y Match 7.3%;
Local Similarity 26.0%;
hes 33; Conservative 1
98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 GGRPPHHPFETKDVSEYSCRELHFTRYVTDGPCRSAKPVTELVCSGQCGPARLLPNAIGR 121
                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: MOST ABUNDANT IN NORMAL LUNG AND MENINGIOMA DISEASE: THE LOSS OF DAN GENE BY MUTATION IS POSSIBLY THE CAUSE THE DEVELOPMENT AND/OR PROGRESSION OF HUMAN NEUROBLASTOMA.
                                                                                                                                                                                                                                                                                                      SIMILARITY: HIGH, TO OTHER MAMMALIAN DAN.
                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: POSSIBLE CANDIDATE AS A TUMOR SUPPRESSOR GENE OF NEUROBLASTOMA. MAY PLAY AN IMPORTANT ROLE IN PREVENTING CEIFROM ENTERING THE FINAL STAGE (G1/S) OF THE TRANSFORMATION
                                                                                                                                                             600613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OR DAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPLGRP--PQSSCTYGALRYERWALWGCPIGSDPRV-LLPVALSCRCAR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity 29.4
32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132
52
159 AA;
                                                                                                         180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
MA SUPPRESSOR OF TUMORIGENICITY 1
                                                                                                                                              DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                        171
19277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 B
52 N
16285 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----CRPINVTVAVEKDECPQCMAVTTTACGGYCRTR----EPVYR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.1%;
                                                                                                         MW.
                                         15;
                                                                                                                     C4-TYPE (PC PRO-RICH.
                                    Score 85; DB Pred. No. 0.45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 94.5; D
Pred. No. 0.05
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
N-LINKED (GLCNAC. . .) (P
52B50C8C879653C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                        15233229DB655865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.5; DB 1;
NO. 0.051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nomura N.,
Iwai J., Yo
                                                                                                                                   (POTENTIAL)
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                                                  DB
0.
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                                                    .45;
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                                         61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yoshida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                     the putative
                                                                Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tabata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .) (POTENTIAL)
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FINGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
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                                        18;
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                                        Gaps
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SYL_MYCLE
ID SYLM
AC Q5019
AC Q5019
AC Q5019
DT 15-JU
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 38
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Q50192;
15-JUL-1998
15-JUL-1998
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eiglmeier K., Garnier T., de Rossi E., Fsihi H., Cole S.T.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-LEUCINE + TRNA(LEU) = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aminoacyl-tRNA synthetase; Protein biosynthesis; SITE 80 89 "HIGH" REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pfam; pF00133; tRNA-synt_1; 1.
prINTS; pR00985; TRNASYNTHLEU.
pROSITE; pS00178; AA_TRNA_LIGASE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y14967; CAA75192.1; -. EMBL; Z70722; CAA94727.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEUCYL-TRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001412; InterPro; IPR002300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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220
                                                     129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYROPHOSPHATE + L-LEUCYL-TRNA(LEU).
SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY
AGERADVIDNCRLVYRADSMVNWCPG
                                                  GPDFRCIPDR----YRAQRVQLLCPG
                                                                                                     TIDVEFYKWTQWIFLQIYNAWFDVAANKARPIAELIAEFDSGERRLVD----GR-DWATLS
                                                                                                                                                        TKDVSEYSCRELHFTRYVT---DGPCRSAKPVTELVCSGQCGPARLLPNAIGRGKWWRPS 128
                                                                                                                                                                                                             TGHNVLHAMGFDAFGLPAEQYAMQTGTHPRILTEA - - NVVNFRHQLGRLGLGHDSRRTFS
                                                                                                                                                                                                                                                                TAFRVVEGQGWQAFKNDATEIIRELGEYPEPPPELENNKTMNRAENG----GRPPHHPFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGTHPHP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGRKPRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEAKNITQIVGHSGC-EAKSIQNRACLGQCF-SYSVPNTF-----PQSTESLVHCDSC
                                                                                                                                                                                                                                                                                                                   ch 7.3%;
l Similarity 26.0%;
38; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR002302; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                    659
972 AA;
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(Rel. 36, Last sequence update)
(Rel. 39, Last annotation updat
SYNTHETASE (EC 6.1.1.4) (LEUCIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
741
744
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745
                                                                                                                                                                                                                                                                                                                                                                                                                                                          108407
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
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                                                                                                                                                                                                                                                                                                                   Score 84.5; I
Pred. No. 3;
L5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "KMSKS" REGION.
ATP (BY SIMILARITY).
GGAEHAVLHL -> AEPNMRCYIC
G; 65286839DA51AFAE CRC6
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                                                     150
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(LEUCINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  972
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                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ligase;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAA94727)
                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                163
                                                                                                        219
                                                                                                                                                                                                                                                                     71
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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                     Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arched:
                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                     Score
    SPTREMBL_16:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhe:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassific
13: sp_vertebrate:
14: sp_virus:*
                                                                                                                                                                                                                                                    Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         November 7, 2001, 16:00:34; Search time 89.34 Seconds (without alignments) 315.435 Million cell updates/sec
    BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                             sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MQLPLALCLICLLVHTAFRV......KPRPRARSAKANQAELENAY 213
                                                                                                                                                                                                                                                                                                                                                              sp_rodent:*
sp_unclassified:*
sp_vertebrate:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_invertebrate;*
sp_mammal:*
    184
215
184
184
492
184
182
184
791
                                                                                                                            11
  3 Q9PWB0
3 Q9PWR2
1 Q8E273
Q9UEM9
Q9HBZ6
Q9HBZ6
Q9HBZ6
1 Q9JKW7
060565
1 Q9FB6
1 Q9FB6
3 Q9FB6
3 Q9FB6
3 Q9FB6
3 Q9FB6
3 Q9FB6
3 Q9FB6
1 Q9FB6
3 Q9FB6
3 Q9FB6
3 Q9FB6
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Q9H772
                                                                                                                                                                                                                                                                                        SUMMARIES
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Oguem9 homo sapien
Og5376 homo sapien
Og9hbz6 homo sapien
Og9hbz7 mus musculu
O60565 homo sapien
Ogmfb6 beta vulgar
O35793 rattus norv
O70326 mus musculu
Og21k6 müs musculu
Og21k6 müs musculu
O73755 gallus gall
O73754 xenopus lae
O9V7U8 drosophila
O70368 rattus norv
P70041 xenopus lae
                                                                                                                                                                          Q9y3u3 homo sapien
Q9h772 homo sapien
Q9hwb0 gallus gall
Q9puk2 gallus gall
Q88273 mus musculu
                                                                                                                                                                                                                                                  Description
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45	44	43	42	41	40	39	38	37	36	35 5	34	သ	32	ω L	30	29	28	27	26	25	24	23	22	21	20
78	78		78.5				79	79	79	79	79.5	79.5	79.5	79.5	80	80	80	80	80	80.5	81	81.5	81.5	81.5	82
6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.9	6.9	6.9	6.9	6.9	6.9	7.0	7.0	7.0	7.0	7.0
224	224	1138	1096	482	365	240	542	355	329	220	1181	1122	1081	500	2531	1440	866	720	712	267	355	1504	1504	1480	988
14	14	10	10	14	Ν	10	N	4	N	10	υī	N	4	10	ъ	5	Çī	4	4	4	4	u	S	U	σ
Q9DJD1	Q9DJD2	Q92PF9	Q9XE24	Q71654	Q52730	Q9SNN5	068872	Q9UJS5	Q9WX60	Q9FP95	Q9V795	085018	076065	Q9м6C2	Q21980	Q20204	P91426	Q9NYZ3	Q9Y557	095813	Q9UKR6	Q9V7F9	Q9XYV4	Q9V7F8	097867
	Q9djd2 foot-and-mo			Q71654 human immun		Q9snn5 oryza sativ		Q9ujs5 homo sapien	Q9wx60 acetobacter	Q9fp95 oryza sativ			076065 homo sapien	Q9m6c2 trifolium r		Q20204 caenorhabdi	P91426 caenorhabdi	homo	homo	O95813 homo sapien	-	Q9v7f9 drosophila		Q9v7f8 drosophila	097867 sus scrofa

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RESULT
Q9PWB0
ID Q9
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Best Local S
Matches 45
heart.".
Curr. Biol. 9:931-938(1999).
EMBL; AF139721; AAD51610.1; -.
InterPro; IPR000359; -.
PR051TE; PS01125; CTCK_2: 1.
SMART; SM00041; CT; 1.
SEQUENCE 272 AA; 31224 MW; 3
                                                                                                                                                                                                                                                                                                    Q9PWB0;
Q9PWB0;
01-MAY-2000
01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9H772 PRELIMINARY; PRT; 168 AA. Q9H772; 01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) CDNA: FLJ21195 FIS, CLONE COL00185.
                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-99439862; PubMed-10508582;
Zhu L., Marvin M.J., Gardiner A.,
                                                                                                                                                                                                                                                                                       CERBERUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
Submilted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK024848; BAB15026.1;
SEQUENCE 168 AA; 19320 MW; D5A4E4E818BF8C0E CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                      "Cerberus regulates left-right asymmetry of the embryonic
                                                                                                                        Levin M.
                                                                                                                                                                                              NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGPARLLPNAIGRGKWWRPSGPDFR----CIPDRYRAQRVQLLCPGGEAP-RARKVRLVA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERWQHQIKEVLASSQEALVVTERKYLKSDWCKTQPLRQTVSEEGCRS-RTILNRECYGQ
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2001 (TrEMBLrel. 16,
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Last sequence update)
Last annotation update)
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                                                                                                                                    A., Lassar A.B., Mercola M.,
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   36E4C9F719711BCA CRC64;
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Best Local S
Matches 32
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T "Carronte, a novel cer-like protein, mediates the establis membryonic left-right asymmetry.";
Nature 0:0-0(1999)
Re EMBL; AFF79484; AAD55581.1; -.
Re InterPro; IPR000359; -.
RINterPro; IPR000359; -.
RR InterPro; IPR001389; -.
RR ProDom; PD000357; -; 1.
RR PROSITE; PS01125; CTCK_2; 1.
R PROSITE; MO0041; CT; 1.
R PROSITE; MO0041; CT; 1.
R SEQUENCE 272 AA; 31201 MW; 0D89729715771BC2 CRC64;
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088273;
088273;
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01-NOV-1998
01-MAR-2001
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Q9PUK2;
Q1-MAY-2000
01-MAY-2000
01-MAR-2001
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Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Caalliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 EPPPELENNK----TMNRAENGGRPPHHPFETKDVSEYSCRELHFTRYVTDGPCRSAKPV 100
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Pred. No. 0.013;
9; Mismatches 58;
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Maximum DB :
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                      score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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score greater than or equal to the score of the result being printed,
1040
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seq length: 2000000000
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| SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MQLPLALCLICLLVHTAFRV.....KPRPRARSAKANQAELENAY 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapext 0.5
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                         AAY96431
AAY96431
AAB26105
AAY96433
AAY96433
                                                                                                                                                                     AAY96430
AAY96436
AAB26106
AAY96429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SE
                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           model
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Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (without alignments)
160.848 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search time 80.28 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   412676
                    Human DAN/Cerberus
Rat TGF-beta bindi
Murine TGF-beta bi
Bovine TGF-beta bi
                                                                                                                    Human DAN/Cerberus
Human TGF-beta bin
Human secreted pro
Vervet TGF-beta bi
                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                         Human TGF-beta bin
Human TGF-beta bin
  Murine
  skin cell
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Sequence of tissue	AAR09290	11	562	7.0	81	45
Sequence of tissue	AAR09288		562	7.0	81	44
Tissue plasminogen	AAP82582		562	7.0	81	3
Homo	AAP50342		562		œ	42
Drosophila SLIT pr	AAR25079		1480	•	81.5	41
	AAB43879	21	150	7.0	82	40
Xenopus cerberus p	AAW41250	19	270	7.1	83	39
T-PA with -ve char	AAR12342	12	561	7.2		38
DAN and b57 protei	AAW29726	19	182	7.4	86.5	37
T-PA with -ve char	AAR13150	12	558	7.5	87	36
EGFP/DRM fusion pr	AAY42178	20	391		87	35
Herpes simplex vir	AAY78333	21	246	7.5	87	34
DAN and b57 protei	AAW29727	19	184	7.5	87.5	33
EGFP/DRM fusion pr	AAY42175	20	429	7.7	90	32
Rat DRM protein se	AAY42174	20	184	7.7	90	31
Human DRM protein	AAY42172	20	184	7.7	90	30
Human gremlin. Ho	AAY95961	21	184	7.9	92	29
DRM	AAY42173	20	184	7.9	92	28
Human b57 protein	AAW69293	19	184	7.9	92	27
Murine cerebral ne	AAY51132	21	168		103	26
Human fetal kidney	AAB10277	21	102	•	104.5	25
Amino acid sequenc	AAY03225	20	102		$\overline{}$	24
Amino acid sequenc	AAY84014	21	168	9.3	108	23
Mutant human TGF-b	AAY96435	21	23		117	22
Human secreted pro	AAW44090	18	116			21
Secreted protein A	AAW27654	18	116		2 2 .	20
Human 5' EST secre	AAY12009	20	50		S	19
Human adult retina	AAB10233	21	206		•	18
Homo sapiens fetal	AAW95711	20	206			17
Human small CCN-li	AAW58704	19	206			16
Human small CCN-li	940	18	206			15
cell prote	597	22	206		•	14
ell protein	5592	22	206	30.2	351.5	13
Murine skin cell p	AAY76031	21	206			

RESULT AAY96430

AAY96430 standard; Protein;

ĄΑ

12-SEP-2000 AAY96430;

(first entry)

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osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; variant; V101; gene therapy; antisense therapy; fracture; chromosome 17q12-21; bone mineralization.
                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                    Human TGF-beta binding protein (BEER) variant V101.
Brunkow ME,
Van Ness J,
                                                                                                                                                                              Homo sapiens
                                              27-NOV-1998;
                                                               24-NOV-1999;
                                                                                  08-JUN-2000.
                                                                                                    WO200032773-A1
                          (DARW-) DARWIN DISCOVERY LTD
Galas DJ,
Winkler DG;
                                              98US-0110283.
                                                                99WO-US27990
                                                                                                                                                 Location/Qualifiers
                                                                                                                       /note= "wild type valine has been substituted with
    isoleucine"
                                                                                                                                         /label= V10I
         Kovacevich B,
         Mulligan JT,
          Paeper BW;
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AAY96436
ID AAY9
XX AAY9
AC AAY9
AC AAY9
AC BEEF
KW OSte
KW BEEF
KW Chrc
XX Home
XX Ho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                               osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; variant; P38R; gene therapy; antisense therapy; fracture; chromosome 17q12-21; bone mineralization.
                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human TGF-beta binding protein (BEER) variant P38R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures
                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY96436 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFGTEAARPQKGRKPRPRARSAKANQAELENAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                           Location/Qualifiers 38
                                                                         /note-
                                                                                                          /label≖ P38R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100
                                "wild type proline has arginine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .08;
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                                                                     been substituted with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB26106
                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 212; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TGF-beta) binding protein designated BEER 938R. The encoded protein comprises a substitution of arginine for the wild-type proline at residue 38. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or vectors may be administered to treat diseases by rectifying mutations or deletions in a patient segment that affect the activity of BEER by expressing inactive proteins or to supplement the patients own production of BEER polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for diagnostic assays and for identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such as a probe of the protein such as the content of the treatment of disorders such as the content of the treatment of disorders such as a probe of the protein such as the
  Human DAN/Cerberus-related protein
                                             15-JAN-2001
                                                                                         AAB26106
                                                                                                                                  AAB26106 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoporosis and fractures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids (I) encoding a transformi protein, useful for identifying agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-NOV-1998;
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                                                                                                                                                                                                                                           dfgteaarpqkgrkprprarsakanqaelenay 213
                                                                                                                                                                                                                                                                                      DFGTEAARPQKGRKPRPRARSAKANQAELENAY 213
                                                                                                                                                                                                                                                                                                                                                                                                                    nggrpphhpfetkdvseyscrelhftryvtdgpcrsakpvtelvcsgqcgparllpnaig
                                                                                                                                                                                                                                                                                                                                                                                                                                             NGGRPPHHPFETKDVSEYSCRELHFTRYVTDGPCRSAKPVTELVCSGQCGPARLLPNAIG
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                                                                                                                                                                                                                                                                                                                             rgkwwrpsgpdfrcipdryragrvgllcpggeaprarkvrlvasckckrltrfhngselk\\
                                                                                                                                                                                                                                                                                                                                                                             RGKWWRPSGPDFRCIPDRYRAQRVQLLCPGGEAPRARKVRLVASCKCKRLTRFHNQSELK 180
                                                                                                                                                                                                                                                                                                                                                    S J,
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Winkler D
                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0110283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US27990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kovacevich B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fractures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a transforming growth factor beta binding fying agents for treating osteopenia,
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                                                                                                                                    213
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Pred. No. 2.7e-105;
1; Mismatches 0;
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Perfect score:
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
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US-09-540-153-7
US-09-540-153-7
US-09-540-153-7
US-09-540-153-7
US-09-540-153-7
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US-08-246-489-2
US-08-246-489-2
US-08-246-489-2
US-08-246-489-7
US-08-484-438-7
US-08-484-438-7
US-08-484-438-7
US-08-486-0-098A-50
US-08-883-795A-38
5118-283-3
    US-08-946-241B-2
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Sequence 159, App
Sequence 26, Appl
Sequence 20, Appli
Sequence 20, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 7, Appli
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Sequence 7, Appli
Sequence 9, Appli
Sequence 38, Appli
Patent No. 5200340
Patent No. 5344773
Sequence 2, Appli
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US-09-188-930-286
Sequence 286, Application US/09188930A; Patent No. 6150502; GENERAL INFORMATION:

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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cel
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEO ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 286
LENGTH: 206
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; ORGANISM: Mouse
US-09-188-930-286
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Best Local Similarity 40.4
Matches 82; Conservative
                                                                                                             APPLICATION NUMBER: US/08/
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                   OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                     ATTORNEY/AGENT INFORMATION: NAME: MULLINS, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hastings, Gregg A. and Adams, Mark D. TITLE OF INVENTION: Human CCN-Like Growth Factor
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32:
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 KWW-RPSGPDFRCIPDRYRAQRVQLLCPGGEAPRARKVRLVASCKCKRLTRFHNQSELKD
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                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
ZIP: 07068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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                           325800-442
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RESULT 4
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          TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 206 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/08468847B Patent No. 5780263 GENERAL INFORMATION:
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Best Local S
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TELEFAX: 201-994-1740
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION NUMBER: US/08/46
APPLICATION NUMBER: US/08/46
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: LII
MOLECULE TYPE:
                                                                                                                                                                                                          APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                          NAME: MULLINS, J.G. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PS/
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 GRPPHHPFETKDVS---EYSCRELHFTRYVTDGPCRSAKPVTELVCSGQCGPARLLPNAI 119
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                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
STRANDEDNESS
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hastings, Gregg A. and Adams, Mark D. VENTION: Human CCN-Like Growth Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINEAR
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8

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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1 MOLPLALCIVCLLVHAAFRV......KPRPRARGAKANQAELENAY 213
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DB
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KTHUB
T10020
T10023
GNNY2F
S71793
S74085
A57534
A57534
A5750
G35070
G37231
VCVWB6
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T183335
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PN0139
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C;Accession: 151373 R;You, S.; Foster, L.K.; Silsby, J.L.; el Halawani, M.E.; Foster, D.N. R;You, S. Foster, L.K.; Silsby, J.L.; el Halawani, M.E.; Foster, D.N. J. Mol. Endocrinol. 14, 117-129, 1995 A;Title: Sequence analysis of the turkey LH beta subunit and its regulation by gonado A;Reference number: 151373; MUID:95290073 A;Accession: 151373 luteinizing hormone beta subunit - turkey C;Species: Meleagris gallopavo (common turkey) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999 C;Accession: I51373 RESULT 151373 R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, submitted to the Protein Sequence Database, March 1999 A;Reference number: Z16471 A;Accession: T08710 hypothetical protein DKFZp564D206.1 - human (fragment) C;Species: Homo sapiens (man) C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999 C;Accession: T08710 C;Acc A;Status: preliminary; translated from GB/EMBL/DDBJ A;MoLecule type: mRNA A;Residues: 1-159 < YOU> A;Cross:references: GB:L35519; NID:g530952; PIDN:AAA74125.1; PID:g530953 A;Molecule type: mRNA A;Residues: 1-134 <MANA A;Cross-references: EMBL.AL050024 A;Experimental source: fetal brain; clone DKFZp564D206 A; Note: DKFZp564D206.1 Matches Query Match Best Local Similarity 122 RKRA 125 196 RPRA 199 136 PDRYRAQRVQLLCPGGAAPRARKVRLVASCKCKRLTRFHNQSELKDEGPEAARPQKGRKP 195 63 NDKTRTQRIQLQCQDGST-RTYKYTVOTACKCKRYTRQHNESSHNFESMSPAKPVQHHRE 121 80 CRELHFTRYVTDGPCRSAKPVTELVCSGQCGPARLLPNAIGRG---KWW-RPSGPDERCI 135 3 CRELRSTKYISDGQCTSISPLKELYCAGECLLLPVLPNWIGGGYGTKYWSRRSSQEWRCV 62 55; Conservative 23.0%; Score 268.5; DB 2 44.4%; Pred. No. 1.1e-16; vative 21; Mismatches 43 DB 2; Length 134; Indels 5; ω

chain

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lutropin beta chain - sperm whale
N;Alternate names: luteinizing hormone beta chain
C;Species: Physeter catodon (sperm whale)
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #:
C;Accession: PN0141
R;Pankov, Y.A.; Karasev, V.S.
Biokhimiia 49, 1004-1018, 1984
A;Title: Luteinizing hormone of the sperm-whale: amin
A;Referepce number: PN0141; MUID:84281133
A;Accession: PN0141
A;Molecule type: protein
A;Polecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Gallus ga
C;Date: 31-Dec 1993
C;Accession: A61091
R;Noce, T; Ando, H.
J. Mol. Endocrinol.
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A,Title: Molecular cloning and nucleotide sequence analysis of the pu A,Reference number: A61091; MUID:89374710
A,Accession: A61091
A,Status: not compared with conceptual translation
A,Molecule type: mRNA
A,Residues: 1-158 <NOC>
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: glycoprotein; hormone; pituitary
F;1-39/Domain: signal sequence #status predicted <SIG>
F;48-73,62-96,65-127,77-149,111-139,129-132/Disulfide bonds: #status
F;48-73,62-96,65-127,77-149,111-139,129-132/Disulfide bonds: #status
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Best I
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Alternate names: luteinizing hormone beta chain
species: Gallus galius (chicken)
;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 SPLGRP--PQSSCTYGALRYERWALWGCPIGSDPRV-LLPVALSCRCARCPIATSDCTVQ
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1-118 <PAN>
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Pred. No. 0.099;
1; Mismatches
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RESULT
PN0139
PN0139
Putropin beta chain - minke whale
N:Alternate names: luteinizing hormone beta chain
C:Species: Balænoptera acutorostrata (minke whale, le:C;Date: 07-May-1993 #sequence_revision 07-May-1993 #te:C;Accession: PN0139
R:Karasev, V.S.; Pankov, V.A.
Biokhimila 50, 1972-1986, 1985
A;Title: Amino acid sequence of reduced and carboxymetl
A:Reference number: PN0138
A:Accession: PN0139
A;Molecule type: protein
A;Residues: 1-118 < KAR>
A;Rote: article in Russian with English abstract
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F40E10.4 - Caenorhabditis elegans C;Speckes: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex C;Accession: T22025
C; Superfamily: pituitary glycoprotein
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A; Residues: 1-601 <WIL>
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A; Accession: T22025
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35; Conservative
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Pred. No. 0.62;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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1169
1 MQLPLALCLVCLLVHAAFRV......KPRPRARGAKANQAELENAY 213
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
          Length
      DΒ
  LSHB_PHYCA
LSHB_BALAC
BCAL_HUMAN
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LSHB_HUMAN
CGHB_HUMAN
CGHB_HUMAN
CGHB_HUMAN
CGHB_HUMAN
CGHB_HUMAN
CGHB_HUMAN
CGHB_HUMAN
CHA_HUMAN
CHA_HUMAN
KLF4_HUMAN
KLF4_HUMAN
KLF4_HUMAN
KLF2_HUMAN
KLF2_HUMAN
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NME3_HUMAN
ENV_FRSFB
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6 meleagris q
bphyseter ca
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5 homo sapien
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7 coturnix co
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EMBL; L35519; AAA74125.1; ALT_INIT. HSSP; P01233; 1HRP. InterPro; IPR001359; InterPro; IPR001345; InterPro; IPR001545; InterPro; IPR002400; Pfam; PP00007; Cys_knot; 1. PROSITE; PR00240; GFCYSKNOT. PROSITE; PS00669; GLYCO_HORMONE_BETA_2; 1. PROSITE; PS00669; GLYCO_HORMONE_BETA_2; 1. HOTMONE; Signal; GlyCO_HORMONE_BETA_2; 1. HOTMONE; Signal; GlyCO_HORMONE_BETA_2; 1. DISULFID 48 96 BY SIMILARITY. DISULFID 48 96 BY SIMILARITY. DISULFID 65 111 BY SIMILARITY. DISULFID 65 121 BY SIMILARITY. DISULFID 73 127 BY SIMILARITY.	s SWISS-PROT entry is copyright. It is produced through ween the SWISS Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restret by non-profit institutions as long as its content ified and this statement is not removed. Usage by and ittes requires a license agreement (See http://www.isb-seend an email to license@isb-sib.ch).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE-Pituitary; MEDLING-9529073; PubMed-7772235; YOU S., FOSTEY L.K., Silsby J.L., el Halawani M.E., FoSTEY D.N.; "Sequence analysis of the turkey LH beta subunit and its regulation by gonadotrophin releasing hormone and prolactin in cultured pituitary cells."; MOI. Endocrinol. 14:117-129(1995). J. MOI. Endocrinol. 14:117-129(1995). J. MOI. FROMOTES SPERMATOGENESIS AND OULLATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS. -!- FUNCTION: PROMOTES SPERMATOGENESIS STEROIDS. -!- SUBGUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN. -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.	Meleagris gallopavo (Common turkey). Meleagris gallopavo (Common turkey). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris. NCBI_TaxID=9103;	01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-BETA) (LSH-B) (LH-B).	RESULT 1 LSHB_MELGA STANDARD; PRT; 159 AA. DC DA56A6.

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Best Local S
Matches 34
PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
HORMONE; G1ycoprotein.
DISULFID 572
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HSSP; P00123; 1HRP.
InterPro; IPR003559; -.
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InterPro; IPR002400; -.
Pfam; PP000007; Cys_knot; 1.
PRINTS; PR00438; GFCYSKNOT.
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B_PHYCA
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P25330;
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Mammalia; Eutheria; (
Physeteridae; Physete
NCBI_TaxID=9755;
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CARBOHYD
SEQUENCE
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BIOKINIT SAME NOT A SEPERMATOGENESIS AND OVULATION BY STIMUL-

PERIOD OF A COMMON ALPHA CHAIN AND A UNIQUE CHAIN WHICH CONTERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.

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01-MAY-1992 (Rel. 22, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
LUTROPIN BETA CHAIN (LUTEINIZING HORMONE BETA
(LSH-B) (LH-B).
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE-87032654; PubMed=3771098;
Pankov Y.A., Karasyov V.S.;
"Primary structure of sperm whale
Int. J. Pept. Protein Res. 28:124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Physeter catodon (Sperm whale) (Physeter macrocephalus)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euto
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti
                                                                                                                                                                                                                                                                                                                                                      MEDLINE-84281133; pubMed-6466737; Pankov Y.A., Karasev V.S.;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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N-LINKED (GLCNAC. . .) (1
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 C SIMILARITY.
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P33088;
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_BALAC
                                                                                 PROSITE;
                                                                                                    InterPro; IPR002400; -.
Pfam; PF00007; Cys_knot; 1.
PRINTS; PR00438; GFCYSKNOT.
                                                                                                                                     PIR; PN0139; PN0139
HSSP; P01233; 1HRP.
InterPro; IPR000359;
                                                                                                                                                                                                                                                                                       Balaenoptera acutorostrata (Minke whale) (Lesser rorqual Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti; Balaenopteridae; Balaenoptera.
NCBI_TaxID=9767;
                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-2090 (Rel. 40, Last annotation update)
LUTROPIN BETA CHAIN (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-BETA)
                                                                                                                                                                                                                                                                                                                                                (LSH-B)
                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
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                                                                                                             rPro; IPR002400;
PF00007; Cys_k
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRFASIRLPGCPPGVNPMV-SFPVALSCHCGPCRLSS-----SDCGPGRAQPLACNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRAQRVQLL-CPGGAAPRARKVRLVASCKCK--RLTRFHNQSELKDFGPEAARPQK-GRK
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Glycoprotein.

9 7 7

D 23 72

D 26 110

26 110

34 88

D 38 90

D 38 90

D 38 10

D 31 13

E 118 AA; 124
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                                                                                  PS00261; GLYCO_HORMONE_BETA_1; PS00689; GLYCO_HORMONE_BETA_2;
                                                                                                                                IPR000359; -. IPR001545; -.
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BY SIMILARITY.
O39F229EFC480F5D CRC64;
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Pred. No.
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ta; Euteleostomi;
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Query Match Best Local S Matches 34

h 7.4%; Similarity 27.6%; 34; Conservative

13;

Score 87; DB Pred. No. 0.23

DB 1

56;

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7;

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Length 118;

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Title:
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                                                                                                                                                                                                                                                             Score
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPTREMBL_16:*
1: sp_archea:*
2: sp_bacteria
                                                                                                                                                                                                                                                           Query
Match Length DB ID
                                 November 7, 2001, 16:00:35; Search time 89.34 Seconds (without alignments) 315.435 Million cell updates/sec
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1169
1 MQLPLALCLVCLLVHAAFRV......KPRPRARGAKANQAELENAY 213
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_archea:*
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sp_fungi:*
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sp_mhc:*
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sp_rodent:*
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sp_vertebrate:*
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O9y3u3 homo sapien
Q9pwb0 gallus gall
O9puk2 gallus gall
O9puk2 gallus gall
Q9h772 homo sapien
Q9uem9 homo sapien
Q88273 mus musculu
Q9xe24 oryza sativ
Q9y557 homo sapien
Q9nyz3 homo sapien
Q9nyz3 homo sapien
Q9nyz3 homo sapien
Q9hbz6 homo sapien
Q9thz7 mus musculu
Q97867 sus scrofa
Q9zik6 mus musculu
Q70326 mus musculu
Q73755 gallus gall
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230	2404	483	470	380	355	270	220	853	853	526	482	1138	365	267	1081	1440	1504	1504	1480	542	381	2531	661	182	791
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Calixxa Hollo Pabiell	nomo	5 mus	Q9unp3 homo sapien	Q9tsv7 sus scrofa	Q9ukr6 homo sapien	P70041 xenopus lae	Q9fp95 oryza sativ	Q9j022 human immun	Q9j023 human immun	·	Q71654 human immun	Q9zpf9 arabidopsis	Q52730 rhizobium e		076065 homo sapien	Q20204 caenorhabdi		09xyv4 drosophila	Q9v7f8 drosophila	O68872 myxococcus	O88995 mus musculu	Q21980 caenorhabdi	Q9v7u8 drosophila	073754 xenopus lae	070368 rattus norv

Qу Db	Qy	Qy Db	Que Bes Mat	A D D R R R R R R O O O O O O D T T T O O O O O O O O O O	RESULT Q9Y3U3
196 RPRA 199 122 RKRA 125	136 PDRYRAQRVQLLCPGGAAPRARKVRLVASCKCKRLTRFHNQSELKDFGPEAARPQKGRKP 195 	80 CRELHFTRYVTDGPCRSAKPVTELVCSGQCGPARLLPNAIGRGKWW-RPSGPDFRCI 135 : :: : : : : :	Query Match 23.0%; Score 268.5; DB 4; Length 134; Best Local Similarity 44.4%; Pred. No. 2.2e-19; Matches 55; Conservative 21; Mismatches 43; Indels 5; Gaps	O993U3; O993U3; OPSTUTEMBLTEL. 12, Created) O1-NOV-1999 (TrEMBLTEL. 12, Last sequence update) O1-NAY-2000 (TrEMBLTEL. 12, Last sequence update) O1-NAY-2000 (TrEMBLTEL. 13, Last annotation update) HYPOTHETICAL 15.3 KDA PROTEIN (FRAGMENT). DKFZP564D206. HOMO Sapiens (Human). BUKARYOta, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; MCBL_TaxID-9606; MCBL_TaxID-9606; FI SUBJEBRAIN; SEQUENCE FROM N.A. TISSUE-BRAIN; SEQUENCE FROM N.A. TISSUE-BRAIN; SUBDUTTER (MAY-1999) to the EMBL/GenBank/DDBJ databases. EMBL; ALOS0024; CAB43243.1; EMBL; ALOS0024; CAB43243.1; EMBL; ALOS0024; CAB43243.1; INCHETER: PS01225; CTCK_2; 1. HYPOTHETICAL DROTEIN. NON_TER 1 1 SEQUENCE 134 AA; 15324 MW; AOB7A8650D2EE6F1 CRC64;	3

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RESULT OF PARTS OF PA
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O9PWB0;
O1-MAY-2000 (TrembLrel.
O1-MAY-2000 (TrembLrel.
O1-MAY-2001 (TrembLrel.
                                                                                                                                                                                                                                                                                                                                                                                                           Q9PUK2;
Q9PUK2;
Q1-MAY-2000
Q1-MAY-2000
Q1-MAR-2001
                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                      Rodriguez Esteban C., Capdevila J., Ortiz A., Izpisua Belmonte J.C.; "Caronte, a novel cer-like protein, embryonic left-right asymmetry."; Nature 0:0-0(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heart.
Curr.
EMBL;
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
EMBL; AF179484; AAD55581.1; IsterPro; IPR000359; - InterPro; IDR001839; - Probom; PD000357; -; 1. PROSITE; PS01225; CTCK_2; 1
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                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           CARONTE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Curr. Biol. 9:931-938(1999).
EMBL; AF139721; AAD51610.1; -
InterPro; IPR000359; -
PROSITE; PS01225; CTCK_2; 1.
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                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
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CE 272 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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31224 MW;
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23.7%;
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Last sequence up
Last annotation
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; Galliformes; Phasianidae; Phasiani
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01-MAR-2001
01-MAR-2001
01-MAR-2001
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Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AKO24848; BAB15026.1; -
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
CDNA: FLJ21195 FIS, CLONE COL00185.
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Mammalia; Eutheria;
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Murine TGF-beta bi
Human DAN/Cerberus
Bovine TGF-beta bi
Human small CCN-li
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Rat DRM protein se	n DRM or	57	Sequence of tissue		hCG/eLH chimera, E	Sequence of tissue	ice of	sm		Human ORFX ORF1506	greml		Human b57 protein	T-PA with -ve char	TBP(20-190)/hCG-be	Caspase 8-interact	T-PA with -ve char	Human ORFX ORF2911	e cer		feta		Mutant human TGF-b	creted pr	prot	n 5′ E	cell	rotein			н	s feta	Human small CCN-li

ALIGNMENTS

osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization.

Vervet TGF-beta binding protein (BEER).

RESULT

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AAY96431;

AAY96431 standard;

Protein;

213

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12-SEP-2000

(first entry)

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AAY96431
ID AAY9
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XX 12-S
XX 12-S
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XW OSTE
KW BEEH
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Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures
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Van Ness J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecus pygerythrus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-NOV-1999;
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                                                                                                                                                                                  2000-412321/35.
DB; AAA29057.
                                                                                                                                                                                                                                                                                                                 Galas DJ, H
Winkler DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0110283.
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                                                                                                                                                                                                                                                                                                                                                                Kovacevich B,
                                                                                                                                                                                                                                                                                                                                                                Mulligan JT,
                                                                                                                                                                                                                                                                                                                                                                     Paeper BW;
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RESULT
AAB26106
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                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                          Human; DNA/Cerberus-related protein 6; hDCR6; morphogenic antagonist; BMP; cell growth; cell differentiation; bone f
                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB26106 standard; Protein; 213 AA
N-PSDB; AAA94051
                WPI; 2000-638179/61
                                                Economides AN,
                                                                                                                       12-MAR-1999;
                                                                                                                                                       02-MAR-2000;
                                                                                                                                                                                          21-SEP-2000
                                                                                                                                                                                                                          WO200055193-A2
                                                                                                                                                                                                                                                                                             gene therapy.
                                                                                                                                                                                                                                                                                                                                                            Human DAN/Cerberus-related protein 6 (hDCR6) (exons 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                   (REGE-) REGENERON PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders such as osteopenia, osteoporosis, fractures and other disorders associated with low mineral content.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGKWWRPSGPDFRCIPDRYRAQRVQLLCPGGAAPRARKVRLVASCKCKRLTRFHNQSELK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MQLPLALCLVCLLVHAAFRVVEGQGWQAFKNDATEIIPELGEYPEPPPELENNKTMNRAE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 100.0%; Score 1169; DB 21; al Similarity 100.0%; Pred. No. 9e-106; 213; Conservative 0; Mismatches 0;
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                                                                                                                                                       2000WO-US05537
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                                                                                                                     99US-0124118
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated, human DNA/Cerberus related protein 6 which include natural homologue, and polypeptides comprising DCR6 domain and nucleids encoding the proteins which are useful as probes and primers
                                                  WPI; 2000-412321/35.
N-PSDB; AAA29055.
                                                                                                                                  Brunkow ME,
Van Ness J,
                                                                                                                                                                                                                                                                    27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                   08-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BEER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        osteopathic; transforming growth factor-beta; TGF-beta; binding protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; antisense therapy; fracture; bone mineralization.
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Nucleic acids (I) encoding a

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Maximum
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Maximum Match 100%
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/Dackfiles1.pep:*
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Gapop 10.0 ,
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-188-930-159
US-09-188-930-286
US-08-910-991-8
US-08-910-991-8
US-09-184-245A-9
US-09-540-245A-7
US-08-96-098A-50
US-08-96-098A-50
US-08-96-166-4
US-08-96-166-4
US-08-96-189B-1
US-08-96-298-189B-1
US-08-91-2-320-12
US-09-142-320-13
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100.150 Million cell updates/sec
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 Sequence 2, Appli
Sequence 159, App
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Sequence 10, Appli
Sequence 11, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 13, Appli
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3 LPLALCLVCLLVHAAFRVVEGQGWQAFKNDATEIIPELGEYPEP-PPELENNKTMNRAEN 61

Matches

83;

Conservative

31;

Mismatches

65;

Indels

26;

Gaps

9;

Query Match 29.8%; Score 348; DB 1; Length Best Local Similarity 40.5%; Pred. No. 3.1e-29; Matches 83: Conservative 31: Mismatches Et. Trace	US-08-468-847B-2 Sequence 2, Application US/08468847B Patent No. 5780263 GENERAL INFORMATION: APPLICAVE: Hastings, Gregg A. and Adams, Mark D. TITLE OF INVENTION: Human CCN-Like Growth Factor NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN, ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD CITY: ROSELAND STATE: NEW JERSEY COUNTRY: USA ZIP: 07068 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER SYSTEM, MS-DOS SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/468,847B FILING DATE: 6 June 1995 CLASSIFICATION NUMBER: US/08/468,847B FILING DATE: 6 June 1995 CLASSIFICATION NUMBER: 33,073 REFERENCE/DOCKET NUMBER: 328800-442 TELEPHONE: 201-994-1704 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 206 AMINO ACIDS TYPE: AMINO ACID STRANDEDNESS: TOPOLOGY: LINEAR NOLECULE TYPE: PROTEIN	28 79.5 6.8 145 4 US-09-142-320-15 29 79.5 6.8 145 4 US-08-918-288-68 30 79.5 6.8 265 4 US-08-918-288-3 31 79.5 6.8 265 4 US-08-918-288-3 32 79.5 6.8 265 4 US-08-918-288-3 34 79.5 6.8 265 4 US-08-282-357-3 34 79.5 6.8 265 4 US-09-282-357-3 35 79 6.8 270 4 US-08-878-474-1 36 79 6.8 470 2 US-08-946-241B-2 37 79 6.8 479 2 US-08-946-241B-2 38 79 6.8 479 2 US-08-946-241B-2 40 78.5 6.7 165 2 US-08-709-928-2 41 78.5 6.7 181 4 US-09-30-928-2 42 78.5 6.7 181 4 US-09-30-282-36-36 43 78.5 6.7 181 4 US-08-282-357-36 44 78 6.7 510 4 US-08-246-489-2 45 77.5 6.6 145 1 US-08-425-673-1
h 206;		Sequence 15, Appl Sequence 68, Appl Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli

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US-08-468-847B-20
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: MULLINS, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hastings, Gregg A. and Adams, Mark D. TITLE OF INVENTION: Human CCN-Like Growth Factor NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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56. GGR--HFSNTGLDRNTRYQVGCRELRSTKYISDGQCTSISPLKELVCAGECLPLPVLPNW 113
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SOFTWARE: WORD PERFECT 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                62 GGRPPHHPFETKDVS---EYSCRELHFTRYVTDGPCRSAKPVTELVCSGQCGPARLLPNA 118
                                                                                                                                                 Local
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                                                                 11 LPLA----CILMKSCL-----AFKNDATEIL--YSHVVKPVPAHPSSNSTLNQARN 55
                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                   3 LPLALCLVCLLVHAAFRVVEGQGWQAFKNDATEIIPELGEYPEP-PPELENNKIMNRAEN 61
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                                                                                                                                                 Similarity
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NEW JERSEY
                                                                                                                                                                                                                                                                                             206 AMINO ACIDS
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                                                                                                                                 Conservative
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                                                                                                                              29.8%; Score 348; DB 1; Length 206; 40.5%; Pred. No. 3.1e-29; tive 31; Mismatches 65; Indels
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                                                                                                                                 Gaps
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; SOFTWARE: FastSEQ

; SEQ ID NO 159

; LENGTH: 206

; TYPE: PRT

; ORGANISM: mouse

US-09-188-930-159
                                                        APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
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SOFTWARE: Fas
SEQ ID NO 286
LENGTH: 206
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                                                                                                                                                                                                                                                                                                                             Sequence 286, Application US/09188930A Patent No. 6150502
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Best Local Similarity 40.3
Matches 80; Conservative
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APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -KWW-RPSGPDFRCIPDRYRAQRVQLLCPGGAAPRARKVRLVASCKCKRLTRFHNQSELK 180
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                                            FastSEQ for Windows Version 3.0
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Pred. No. 5.1e-29;
1; Mismatches 66
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MUC5B, trach

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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296.219 Million cell updates/sec
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                                                                                                                                                                                                                        fact
Intropin beta chain - sperm whale

N; Alternate names: luteinizing hormone beta chain
C; Species: Physeter catodon (sperm whale)
C; Date: 07-May-1993 #sequence_revision 07-May-1993 #text_C
C; Accession: PN0141
R; Pankov, Y.A.; Karasev, V.S.
Biokhimia 49, 1004-1018, 1984
A; Title: Luteinizing hormone of the sperm-whale: amino aci
A; Reference number: PN0141; MUID:84281133
A; Accession: PN0141
A; Molecule type: protein
A; Residues: 1-118 <PAN>
A; Note: article in Russian with English abstract
C; Superfamily: pituitary glycoprotein hormone beta chain
C; Keywords: glycoprotein; hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein DKFZp564D206.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08710
R;Wambutt, R; Heubner, D; Mewes, H.W.; Gassenhuber, J; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z16471
A;Accession: T08710
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T08710
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A:Residues: 1-134 <WAM>
A:Cross-references: EMBL:AL050024
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Best Local (
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                                                                                                                                                                                                                                                                                                          194 RPGARGAKANO 204
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52; Conservative
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                     beta chain
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R; You,
J. Mol.
                                                          lutropin beta chain - minke whale

N;Alternate names: luteinizing hormone beta chain
C;Species: Balaenoptera acutorostrata (minke whale,
C;Date: 07-May-1993 #sequence_revision 07-May-1993
C;Accession: PN0139
C;Accession: PN0139
C;Accession: PN0139
C;Karasev, V.S.; Pankov, Y.A.
Biokhimila 50, 1972-1986, 1985
A;Title: Amino acid sequence of reduced and carboxy
A;Reference number: PN0138
                                                                                                                                                                                                               PNO139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-159 <YOU>
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A; Molecule type: protein A; Residues: 1-118 <KAR> A; Note: article in Russi
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C;Superfamily: pituitary glycoprotein hormone beta chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Sequence analysis of the turkey LH beta subunit A; Reference number: I51373; MUID:95290073 A; Accession: I51373
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Species: Meleagris gallopavo (common turkey)
Date: 13-Sep-1996 #sequence_revision 13-Sep-1996
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                                                                                                                                                                                                                                                                                                                                           SPIGRP--PQSSCTYGALRYERWALMGCPIGSDPRV-LLPVALSCRCARCPIATSDCTVQ 142
                                                                                                                                                                                                                                                                                                                                                                              VKWWRPNGPDFRCIPDRYRAQRVQLL-CPGGAAPRSRKVRLVASCKCKRLTRFHNQSELK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPG 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRPINATLAAQNZACPVCITFTTSICAGYCPSMVRVLPAAL-----PPVPZPVCTYRQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRELHYTRELTDGPCRSAKPVTELVCSGQC-GPARLLPNAIGRVKWWRPNGPDFRCIPDR 136
                                                                                                                                                                                                                                                                                                                                                                                                          GGRPP-----CRPINVTVAVEKDECPQCMAVTTTACGGYCRTR----EPVYR 85
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37; Conserv
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English abstract
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Pred. No. 0.3;
l3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 92.5; DB Pred. No. 0.45;
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ribosomal protein L2 - evening primrose mitochondrion () Species: mitochondrion Oenothera villaricae (evening primrose) () Date: 27-Jan-1995 #sequence_revision 24-Feb-1995 #text_change 13-Aug-1999 () Accession: $46947 submitted to the EMBL Data Library, July 1994 A; Reference number: $46947 A; Reference number: $46947 A; Recession: $46947
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N;Alternate names: luteinizing hormone beta chain
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
C;Accession: A61091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: pituitary glycoprotein hormone beta chain C;Reywords: glycoprotein; hormone; pituitary F:1-39/Domain: signal sequence *status predicted <SIG>F:48-73,62-96,65-127,77-149,111-139,129-132/Disulfide bonds: *status F:52/Binding site: carbohydrate (Asn) (covalent) *status predicted
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A; Residues: 1-158 < NOC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARLLPNAIGRVKWWRPNGPDFRCIPDRYRAQRVQLL-CPGGAAPRSRKVRLVASCKCKR 167
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32; Conserv
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6 bluetongue
9 bluetongue
9 bluetongue
8 homo sapien
4 struthio ca
2 xenopus lae
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6 mus musculu
2 homo sapien
5 brassica na
4 drosophila
9 chironomus
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Query Match

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the Euro
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YOU S., FOSter L.K., Silsby J.L., el Halawani M.E.,
"Sequence analysis of the turkey LH beta subunit and
by gonadotrophin-releasing hormone and prolactin in
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HSSP; P01233; 1HRP.
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European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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                                                                                  Signal;
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Meleagrididae; Meleagris.
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Best Local
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01-0CT-1993
01-0CT-2000
                                   DISULFID
DISULFID
               CARBOHYD
SEQUENCE
                                                                   DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                  "Amino acid sequence of reduced and subunits of the little picked whale Biokhimiia 50:1972-1986(1985).
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Cetartioda Balaenopteridae; Balaenoptera. NCBI_TaxID=9767;
                                                                                                            pfam: pF00007; Cys_knot; 1.
prints; pR00438; GFCYSKNOT.
pROSITE; pS00261; GLYCO_HORMONE_BETA_1;
pROSITE; pS00689; GLYCO_HORMONE_BETA_2;
                                                                                                                                                                                                                                                                                                                                                                                                               LUTROPIN BETA CHAIN (LUTEINIZING HORMONE (LSH-B) (LH-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSHB_BALAC P33088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BALAC
                                                                                                                                                                                      PIR; PN0139; PN0139.
HSSP; P01233; 1HRP.
                                                                                                   Hormone;
                                                                                                                                                                   InterPro;
                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           Balaenoptera
                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 GLGP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 DFGP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 GGRPPHHPYDAKDVSEYSCRELHYTRFLTDGPCRSAKPVTELVCSGQCGPARLLPNAIGR 119
                                                                                                                                                                                                            SIMILARITY: FAMILY.
                                                                                                                                                                                                                 FUNCTION: PROMOTES SPERMATOGENESIS AND THE TESTES AND OVARIES TO SYNTHESIZE ST SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN WHICH CONFERS BIOLOGICAL SPECIFIC LUTROPIN, FOLLITROPIN AND GONADOTROPIN. SIMILARITY: BELONGS TO THE GLYCOPROTEIN FORLYTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPLGRP--PQSSCTYGALRYERWALWGCPIGSDPRV-LLPVALSCRCARCPIATSDCTVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKWWRPNGPDFRCIPDRYRAQRVQLL-CPGGAAPRSRKVRLVASCKCKRLTRFHNQSELK
1233; 1HRP.
; IPR000359; -.
; IPR001545; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 26.0
33; Conservative
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159
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etazoa; Chordata; Craniata; Vertebrata; Eute
theria; Cetartiodactyla; Cetacea; Mysticeti;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    27, Created)27, Last sequence up40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52
16285 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.9%;
26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -CRPINVTVAVEKDECPQCMAVTTTACGGYCRTR----EPVYR
               MW;
             BY SIMILARITY.
O-1.1100 (GLCNAC...).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                      GLYCOPROTEIN
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No. 0.
                                                                                                                                                                                                                                         HESIZE STEROIDS.
ON ALPHA CHAIN AND A UNIQUE
SPECIFICITY TO THYROTROPIN,
                                                                                                                                                                                                                                                                                             carboxymethylated luteinizing hormor
                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                      HORMONES BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT) (LSH-BETA)
                                                                                                                                                                                                                                                                                               hormone
                                                                                                                                                                                                                                                                                                                                                                                 rorqual).
;a; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 159;
                                                                                                                                                                                                                                                                                               d alpha-
one.";
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                                                                                                                                                                                                                                                                                                         beta-
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Query Match Best Local Matches 3

36;

Conservative

12;

Mismatches

57;

Indels

18;

Gaps

6;

Similarity

7.8%; 29.3%;

Score 91; Pred. No.

0.1

.13;

Length 118;

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rched:
      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                   249.5
90.5
                                                                                                                                                                                                                                    Score
                                     88.5
88.5
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68
68
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Match Length DB
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1171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_archea:*
sp_bacteria:*
sp_fungi:*
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sp_phage:*
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sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                          sp_virus:*
                                                                                                                                                                                                                                                                                                                                                     sp_unclassified:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                            sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                       sp_plant:*
                                                           720
988
215
261
262
182
184
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184
281
332
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13 073755
4 09Y575
4 09YZ3
6 09/B67
8 09WB6
2 09FL6
2 09FL6
13 073754
4 060565
11 035793
   070326
Q9H772
Q9PUK2
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Q40600
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                                    Q9PWB0
Q71654
Q9JKW7
                                                                                                                                                                                                                                                                       SUMMARIES
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Q9y3u3 homo sapien
073755 gallus gall
09y557 homo sapien
09y867 sus scrofa
09mf26 beta vulgar
09f164 acetobacter
013091 pleurodeles
073754 xenopus lae
060565 homo sapien
035793 rattus norv
09ewd9 streptomyce
040600 cenothera b
09pwb0 gallus gall
071654 human immun
09jkW7 mus musculu
09h772 homo sapien
                                                                                                                                                                                                                                    Description
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Qy 194 RPGARGAKANQ 204 : ::: Db 122 RKRASKSSK 130	
QY 134 PDRYRAORVOLLCPGGAAPRSRKVRLVASCKCKRLTRFHNQSELKDFGPETARPQKGRKP 193	
Qy 78 CRELHYTRFLTDGPCRSAKPVTELVCSGQCGPARLLPNAIGRVKWW-RPNGPDFRCI 133	
Query Match 21.3%; Score 249.5; DB 4; Length 134; Best Local Similarity 39.7%; Pred. No. 2.3e-17; Matches 52; Conservative 28; Mismatches 44; Indels 7; Gaps	
RY [1] RY SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.; RA Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. DR InterPro; IPR000359; DR InterPro; IPR000359; DR PROSITE; PS01225; CTCK_2; 1. KW Hypothetical protein. KW Hypothetical protein. FT NON_TER 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
RESULT 1 Q9Y3U3 ID Q9Y3U3 PRELIMINARY; PRT; 134 AA.	

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RESULT
ID 37755
ID 37757
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SEQUENCE
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Gallus g
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DJ1163J1.3 (NOVEL PROTEIN SIMILAR TO MOUSE B99) (FRAGMENT).
DJ1163J1.3.
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MEDITAN=98325381; PubMed=9660951;

HSU D.R., Economides A.N., Wang X., Eimon P.M., Harland R.

"The Xenopus dorsalizing factor Gremlin identifies a novel secreted proteins that antagonize BMP activities.";

Mol. Cell 1:673-683(1998).

EMBL; AF045799; AAC41280.1; -.

Interpro; IPR000359; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9Y557
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SEOUENCE 184 AA;
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01-AUG-1998 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lloyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
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                                                                   91: PCRSAKPVTELVCSGQCGPARLLP----NAIGRVKWWRPNGPDFRCIPDRYRAQRV---- 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEYPEP----PPENNQTMNRAENGGRPPHH----PYDAKDVSEYSCRELHYT--RFLTDG
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   PANSSRPLSNISKSGRMGPAMLRPALPAGPVGASSW--
                                                                                                                                                                                                                                                                                                                                        AL031588; CAB38415.1; -.

ER 1 1
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ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                          Similarity 22. 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                     712 AA;
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                                                                                                                                                                                                                                                                                                                         75685 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21166 MW;
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16,
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Last sequence update)
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Pred. No. 0.83
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097867;
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01-MAY-1999;
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Q9NYZ3;
01-OCT-2000
01-OCT-2000
01-OCT-2000
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Sus scrofa domestica (domestic pig).
Sus scrofa domestica (domestic pig).
Chordata; Craniata; Vertebrata;
Chordata; Craniata; Vertebrata;
Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monte M., Collavin L., Lazarevic D., Utrera R., Schneid "Cloning, Chromosome mapping and functional characteriz human homolog gene of murine B99.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF223408; AAF31459.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B99
                     Biochem. J. 308:0-0(0)
                               "Isolation mucin.";
                                                               MEDLINE=95275264; PubMed=7755593;
Turner B.S., Bhaskar K.R., Hadzop
                                                                                     SEQUENCE OF 35-109 FROM N. TISSUE=GASTRIC EPITHELIUM;
                                                                                                                                                                              GASTRIC MUCIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Mammalia; Eutheria;
                                                                                                                        NCBI_TaxID~9825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                       LaMont J.T.
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1 (TrEMBLrel. 16,
                                          and characterization
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Primates;
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                                                                 Hadzopoulou-Cladaras
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                                          pig gastric
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SEQUENCE

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Human TGF-beta bin
Human DAN/Cerberus
Bovine TGF-beta bi
Murine skin cell p
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Rat TGF-beta bindi
Vervet TGF-beta bi
Human DAN/Cerberus
Human TGF-beta bin
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AAG35060 AAB88367	AAG20508	35C	AAG20509	AAR15109	σ	AAW99515	AAY51132	101	AAY83261	16	AAY42172	AAY42178	17	17	596	AAY42173	AAW69293	AAW29726	31	AAW29727	AAB10277	AAY03225	AAW44090	AAW27654	0	AAB10233	AAW95711	AAW58704	AAW09408	9	AAB55920	AAY76031
Arabidopsis thalia Human membrane or		Arabidopsis thalia	Arabidopsis thalia	imera,	Fragmented human N	Glycoprotein hormo	Murine cerebral ne	o acid	HSV-1 V22 cellular	Human ORFX ORF2933	—	EGFP/DRM fusion pr		Rat DRM protein se	Human gremlin. Ho	Mouse DRM protein		DAN and b57 protei	in ORFX ORF291	nd b57			sec	Secreted protein A	~	retin	Ω.	small CCN-l	n small	cell prote	ell protein	Murine skin cell p

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RESULT
AAY96432
  Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures
                                         WPI; 2000-412321/35.
N-PSDB; AAA29058.
                                                                                                                                                                                                            Mus musculus.
                                                                                                                                                                                                                               osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization.
                                                                                                                                                                                                                                                             Murine TGF-beta binding protein (BEER).
                                                                                                                                                                                                                                                                                   12-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                         AAY96432;
                                                                       Brunkow ME,
Van Ness J,
                                                                                                                            27-NOV-1998;
                                                                                                                                                24-NOV-1999;
                                                                                                                                                                     08-JUN-2000.
                                                                                                                                                                                       WO200032773-A1.
                                                                                                                                                                                                                                                                                                                             AAY96432 standard;
                                                                                                      (DARW-) DARWIN DISCOVERY LTD.
                                                                       Galas DJ,
Winkler DG;
                                                                                                                           98US-0110283.
                                                                                                                                                99WO-US27990.
                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                  Kovacevich B,
                                                                                                                                                                                                                                                                                                                              211
                                                                                   Mulligan
                                                                                   JT,
                                                                                  Paeper BW;
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RESULT
AAY96433
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N-PSDB; AAA29059
                                        Brunkow ME,
Van Ness J,
                                                                                                                                                                                                                                                                                                                12-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                WPI; 2000-412321/35
                                                                                                             27-NOV-1998;
                                                                                                                                    24-NOV-1999;
                                                                                                                                                               08-JUN-2000
                                                                                                                                                                                          W0200032773-A1
                                                                                                                                                                                                                    Rattus norvegicus
                                                                                                                                                                                                                                               BEER;
                                                                                                                                                                                                                                                           osteopathic;
                                                                                                                                                                                                                                                                                      Rat TGF-beta
                                                                                                                                                                                                                                                                                                                                           AAY96433;
                                                                                                                                                                                                                                                                                                                                                                    AAY96433 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders such as osteopenia, osteoporosis, fractures and other disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KWWRPNGPDERCIPDRYRAQRVQLLCPGGAAPRSRKVRLVASCKCKRLTRFHNQSELKDF
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                                                                                  DARWIN DISCOVERY LTD
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                                                                                                                                                                                                                                            therapy;
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                                         Galas DJ,
Winkler DG
                                                                                                                                                                                                                                                           transforming growth factor-beta; TGF-beta; binding protein;
                                                                                                                                                                                                                                                                                      binding
                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                           98US-0110283
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                                                       Kovacevich
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Pred. No. 5.5e-100;
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                                                       В,
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RESULT
AAY96431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This shows a rat transforming growth factor-beta (TGF-beta) binding protein designated rBEER. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or
                                                                                                                                                                                       Cercopithecus pygerythrus
                                                                                                                                                                                                                                         osteopathic;
                                                                                                                                                                                                                                                                                                                                                                   AAY96431 standard; Protein; 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vectors may be administered to treat diseases by rectifying mutations deletions in a patient's genome that affect the activity of BEER by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 125-126; 162pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures
                               (DARW-) DARWIN DISCOVERY LTD
                                                                                                                            08-JUN-2000
                                                                                                                                                           WO200032773-A1
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                                                              27-NOV-1998;
                                                                                              24-NOV-1999;
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                                                                                                                                                                                                                       gene therapy;
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                                                                                                                                                                                                                                         transforming growth factor-beta;
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                                                              98US-0110283.
                                                                                              99WO-US27990
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93.9%;
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                                                                                                                                                                                                                       therapy; fracture; bone
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                                                                                                                                                                                                                                       binding protein;
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Brunkow ME,

Galas DJ,

Kovacevich

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Mulligan JT,

Paeper

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is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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Sequence 159, App
Sequence 286, App)
Sequence 2, Applil
Sequence 21, Applil
Sequence 2, Applil
Sequence 3, Applil
Sequence 9, Applil
Sequence 5, Applil
Sequence 5, Applil
Sequence 5, Applil
Sequence 7, Applil
Sequence 3, Applil
                                                                                                                                                                                                                                                                                                                                                                                                                Description
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APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew

APPLICANT: Sleeman, Matthew

APPLICANT: Orrust, Rene

APPLICANT: Orrust, Rene

APPLICANT: Murison, James Greg

TITLE OF INVENTION: Compositions Isolated From Skin Cells

TITLE OF INVENTION: and Methods For Their Use

FILE REFERENCE: 11000,1011c1

CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 348

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 159

LENGTH: 206

TYPE: PRT
US-09-188-930-286
Sequence 286, Septication US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
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Best Local S
Matches 80
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                                                                                                                              ELKDFGPETARPQKGRKPRPGARGAKANQAEL 207
                                                                                                                                                                                                                       --HFSSTGLDRNSRVQVGCRELRSTKYISDGQCTSISPLKELVCAGECLPLPVLPNWIGG
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                                                                                                                                                                                                                                                                               SLIP-LLCILMRNCL-----AFKNDATEILYSHVVKPVPAHPSSNSTLNQARNGGR
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37.7%;
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US-08-475-213-10
US-08-475-213-20-12
US-09-142-320-12
US-09-142-320-13
US-09-142-320-15
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US-08-918-39-36-39
US-08-918-39-36-39
US-08-918-39-38
US-08-918-39-38
US-08-918-39-38
US-08-918-39-38
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Pred. No. 8.9e-28;
8; Mismatches 71;
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Sequence 2, Applil
Sequence 2, Applil
Sequence 12, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 68, Appli
Sequence 68, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 8, Appli
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9;

Minimum Maximum

BG

seq

length:

0 20000000000

Total number

of

hits satisfying chosen parameters:

212252

212252 seqs, 22503292 residues

Database

Issued_Patents_AA:*

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2: /cgn2_6/ptodata/2,

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/cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Result

Score

Query Match

Length

DB

SUMMARIES

340.5 340.5 333 333

206 206 206 206 206 201 301 301 470 470 470 270 270

Pred. No. score grea and is der

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US-09-188-930-159
US-09-188-937-286
US-08-468-847B-20
US-08-368-364-21
US-08-303-86-21
US-08-303-11444-2
US-08-4711-3-3
US-09-191-647-3
US-09-191-647-3
US-09-191-647-3
US-09-191-647-3
US-09-413-8-1
US-08-403-427A-5
US-08-403-427A-7
US-08-469-427A-7
US-08-469-427A-7
US-08-469-427A-7
US-08-469-427A-7
US-08-469-427A-3
US-08-469-427A-3
US-08-69-0632-3
US-08-69-0632-3
US-08-69-0632-3
US-08-69-0632-3
US-08-69-0632-3
US-08-69-0632-3

735 735 1213 188 188 188 195 195 195 55

Title: Perfect

score:

US-09-668-021-12 1171

MQPSLAPCLICLLVHAAFCA...

....KPRPGARGAKANQAELENAY

Sequence:

ş

protein on

protein search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Comp

Compugen Ltd

November

7, 2001, 15:47:17

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Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0

8;

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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Aatthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REPERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
TYPE: PRT
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08468847B Patent No. 5780263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                              APPLICATION NUMBER: US/08/
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tches
ATTORNEY AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32!
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hastings, Gregorithm of INVENTION: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 SHNFESVSPAKPAQHHRER--KRASKSSKHSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 ELKDFGPETARPQKGRKPRPGARGAKANQAEL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 GYGTKYWSRRSSQEWRCVNDKTRTQRIQLQCQDGST-RTYKITVVTACKCKRYTRQHNES 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 -- RVKWW-RPNGPDFRCIPDRYRAQRVQLLCPGGAAPRSRKVRLVASCKCKRLTRFHNQS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6 BECKER I
CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 --HFSSTGLDRNSRVQVGCRELRSTKYISDGQCTSISPLKELVCAGECLPLPVLPNWIGG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 PPHHP---YDAKDVSEYSCRELHYTRFLTDGPCRSAKPVTELVCSGQCGPARLLPNAIG- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 80; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLIP-LICILMRNCL-----AFKNDATEILYSHVVKPVPAHPSSNSTLNQARNGGR 58
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                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                       INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gregg A. and Adams, Mark D.
Human CCN-Like Growth Factor
                                                                                                                                                                                                                                   US/08/468,847B
                               325800-442
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RESULT 4
US-08-468-847B-20
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Best Local S
Matches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/084688478 Patent No. 5780263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                          TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 0 LL.
STREET: NOSELAND
CTATE: NEW JERSEY
                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32.22
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: (FILING DATE: 6 June CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hastings, Gregg A. and Adams, Mark D. TITLE OF INVENTION: Human CCN-Like Growth Factor NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: LI
                                                     SEQUENCE CHARACTERISTICS:
                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 SMSPAKPVQHHRER--KRASKSSK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 YWSRRSSQEWRCVNDKTRTQRIQLQCQDGST-RTYKITVVTACKCKRYTRQHNESSHNFE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 WW-RPNGPDFRCIPDRYRAQRVQLLCPGGAAPRSRKVKLVASCKCKRLTRFHNQSELKDF 180
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PS/2
OPERATING SYSTEM: 1
                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 YDAKDVS---EYSCRELHYTRFLTDGPCRSAKPVTELVCSGQCGPARLLPNAIG---RVK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 LACILMKSCL-----AFKNDATEILYSHVVKPVPAHPSSNSTLNQARNGGR--HFS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 37.3 nes 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 206 AMINO ACIDS TYPE: AMINO ACID
STRANDEDNESS
                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 LICLLVHAAFCAVEGQGWQAFRNDATEVIPGLGEYPEPP-PENNQTMNRAENGGRPPHHP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPETARPQKGRKPRPGARGAKANQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTGLDRNTRVQVGCRELRSTKYISDGQCTSISPLKELVCAGECLPLPVLPNWIGGGYGTK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07068
                  AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 BECKER FARM ROAD
                                     206 AMINO ACIDS
                                                                                             201-994-1744
                                                                                                                                                                                                                                                                                                                                                                    WORD PERFECT 5.1
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                                                                                                                                                                                                                                                                                                          6 June 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.4%; Score 333; DB 1; Length 206; 37.3%; Pred. No. 5.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                       MS-DOS
                                                                                                                                                                                                                                                                                                                               US/08/468,847B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                       325800-442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67;
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Run on:
                                                                                                                                                  OM protein - protein search, using sw model
US-09-668-021-14
1167
                                                             November 7, 2001, 15:49:47; Search time 54.26 Seconds (without alignments) 299.027 Million cell updates/sec
                                                                                                                                                                                                                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Title: Perfect score:

1 MQLSLAPCLACLLVHAAFVA.....KPRPRARGAKANQAELENAY.213

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 219241 seqs, 76174552 residues

219241

Minimum DB Maximum DB seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	S	5	4	w	2		No.	Result
75	75.5	75.5	76	76	76	76.5	76.5	76.5	77	77	77	77.5	77.5	77.5	78	78.5	79.5		80	80	81	2	82.5	86	88	92.5	95.5	6.	Score	
6.4	6.5	6.5	6.5	6.5	6.5	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.7	6.7	6.8	6.9	6.9	6.9	6.9	7.1	7.1	7.4	7.5	7.9	8.2	22.0	1	Ouerv
379	705	128	1589	765	269	1223	301	145	1682	1480	385	368	270	188	343	2098	165	3161	2142	601	3163	1469	166	118	118	158	159	134	Length	
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A35669	T22201	S74085	T42233	T49592	D75631	S29717	WMBEF9	137231	C70588	A36665	A54039	S67507	S71793	JC4680	G35070	T18397	KTHUB	T30342	в35098	T22025	T17440	в36665	151242	PN0139	PN0141	A61091	I513 7 3	T08710	ID	
gene CYR61 protein	hypothetical prote	lutropin beta chai	submaxillary mucin	neurofilament trip	iron ABC transport	adenylate cyclase	UL49 protein - hum	beta-gonadotropin	probable mbtE prot	slit protein 1 pre	major surface prot	morphogen lefty pr	head-inducing fact	vascular endotheli		protein CTRP - mal	choriogonadotropin	protein HMWP1 - Ye	MHC class III hist	hypothetical prote	probable polyketid	slit protein 2 pre	luteinizing hormon		lutropin beta chai	lutropin beta chai		al pro	Description	

Luteinizing hormone beta subunit - turkey
C;Species: Meleagris gallopavo (common turkey)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999 .
C;Accession: 151373
R;You, S:; Foster, L.K.; Silsby, J.L.; el Halawani, M.E.; Foster, D.N.
J. Mol. Endocrinol. 14, 117-129, 1995
A;Title: Sequence analysis of the turkey LH beta subunit and its regulation by gonado A;Reference number: 151373; MUID:95290073
A;Accession: 151373
A;Accession: 151373
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-159 <YOU>
A;Cross-references: GB:L35519; NID:g530952; PIDN:AAA74125.1; PID:g530953
C;Genetics:

A; Gene: LH-beta

45	44	43	42	41	40	39	88	37	36	<u>ω</u> 5	34	ω 3	32	31	30 .
73	73	73.5	73.5	73.5	73.5	73.5	73.5	74	74	74	74.5	74.5	75	75	75
6.3	6.3	6.3	6. ₃	6.ω	6.3	6.3	6.3	6.3	6. ₃	6. ₃	6.4	6.4	6.4	6.4	6.4
332	305	3133	1436	1042	324	324	270	721	563	174	866	322	450	405	383
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S46947	S22313	S52093	A46496	A57534	JQ2292	139382	A83501	T45495	A36054	BQIC1T	T29197	I58195	G01158	S33601	A23516
ribosomal protein	B box-binding prot	hemocytin - silkwo	antigen WC1.1 prec	mucin 5AC (clone L	Y box-binding prot	Y box-binding prot	conserved iypothet	probable transposa	mucin homolog - bo	Balbiani ring-1 ch	hypothetical prote	Y box-binding prot	tyrosine kinase ac	cell adhesion mole	Balbiani ring 1 ch

ALIGNMENTS

hypothetical protein DKFZp564D206.1 - human (fragment) C;Species: Homo saplens (man) C;Species: Homo saplens (man) C;Species: Toun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999 C;Accession: T08710 C;Accession: T08710 C;Accession: T08710 C;Accession: T08710 C;Accession: T08710 A;Reference number: Z16471 A;Accession: T0870 A;Reference number: Z16471 A;Accession: T08710 A;Molecule type: mRNA A;Residues: 1-134 <mam> A;Residues: 1-134 <mam 1-134="" <mam="" a;residue<="" a;residues:="" th=""></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam></mam>
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lutropin beta chain - sperm whale
N;Alternate names: luteinizing hormone beta chain
C;Species; Physeter catodon (sperm whale)
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #
C;Accession: PN0141
C;Accession: PN0141
R;Pankov, Y.A.; Karasev, V.S.
Bickhimila 49, 1004-1018, 1984
A;Title: Luteinizing hormone of the sperm-whale: ami
A;Referense number: PN0141; MUID:84281133
A;Accession: PN0141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Noce, T; Ando, H; Ueda, T; Kubokawa, K; Higashinakagawa, T; Ishii, S.
J. Mol. Endocrinol. 3, 129-137, 1989
A; Title: Molecular cloning and nucleotide sequence analysis of the putative cDNA for the A; Reference number: A61091; MUID:89374710
A; Accession: A61091
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-158 < NOC>
C; Superfamily: pituitary glycoprotein hormone beta chain
C; Keywords: glycoprotein; hormone; pituitary predicted <SIG>
F; 48-73,62-96,65-127,77-149,111-139,129-132/Disulfide bonds: #status predicted
F; 52/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                RESULT
PN0141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Galius yo
C;Date: 31-Dec-1993
C;Accession: A61091
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A; Molecule
A; Residues:
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Date: 31-Dec-1993 #sequence_revision 31-Dec-1993
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Pred. No. 0.36
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A;Accession: PN0139
A;Molecule type: protein
A;Residues: 1-118 <KAR>
A;Note: article in Russian with English abstract
C;Superfamily: pituitary glycoprotein hormone bet
C;Keywords: glycoprotein; hormone
C;Keywords: glycoprotein; hormone
F;9-34,23-57,26-88,38-110,72-100,90-93/Disulfide
F;13/Binding site: carbohydrate (Asn) (covalent)
                                              R;Ando, H.; Ishii, S.
Gen. Comp. Endocrinol. 93,
A;Title: Molecular cloning
                                                                                                                                                    luteinizing hormone beta-subunit - quail
C;Species: Coturnix coturnix (quail)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996
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A;Title: Amino acid sequence
A;Reference number: PN0138
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Pred. No. 0.67
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A;Note: article in Russian with English abstract C;Superfamily: pituitary glycoprotein hormone bet C;Keywords: glycoprotein; hormone F;9-34,23-57,26-88,38-110,72-100,90-93/Disulfide F;13/Binding site: carbohydrate (Asn) (covalent)
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Interpro; IPRO02400; ...

PETAM; PFO0007; Cys_knot; 1.

PRINTS; PRO0438; GEYCXSKNOT.

PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.

PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.

PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.

PROSITE; PS00689; GLYCO_HORMONE_BETA_1; 1.

PROSITE;
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ALIGNMENTS

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Ü	LSHB_MELGA STANDARD; PRT; 159 AA.
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ij	01-OCT-2000 (Rel. 40, Last annotation update)
ĕ	LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-
Ħ	BETA) (LSH-B) (LH-B).
ž	LHB.
Š	Meleagris gallopavo (Common turkey).
გ	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
റ്	Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
×	NCBI_TaxID=9103;
ĩ	[1]
õ	SEQUENCE FROM N.A.
റ്	TISSUE=Pituitary;
×	MEDLINE=95290073; PubMed=7772235;
õ	You S., Foster L.K., Silsby J.L., el Halawani M.E., Foster D.N.;
ã	"Sequence analysis of the turkey LH beta subunit and its regulation
~	by gonadotrophin-releasing hormone and prolactin in cultured
ã	pituitary cells.";
ñ	
റ്	-!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
റ്	THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
റ്	-!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
റ്	CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
റ്	LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
റ്	-!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
ñ	FAMILY.
റ്	
ä	This SWISS-PROT entry is copyright. It is produced through a collaboration
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റ്	the European Bioinformatics Institute. There are no restrictions on its
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ದ	entities requires a license agreement (See http://www.isb-sib.ch/announce/
റ്	or send an email to license@isb-sib.ch).
Ö	
¥	EMBL; L35519; AAA74125.1; ALT_INIT.
Ħ	HSSP; PULZ33; THRP.

POTENTIAL.
LUTROPIN BETA CHAIN.
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Best Local
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 Hormone;
DISULFID
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01-MAY-1992
01-OCT-2000
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                              Biokhimiia 49:1004-1018(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87032654; PubMed=3771098; Pankov Y.A., Karasyov V.S.; "Primary structure of sperm whale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Physeter catodon (Sperm whale) (Physeter macrocephalus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSHB_PHYCA
P25330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _РНҮСА
                                                                                                              PROSITE;
                                                                                                                              PROSITE;
                                                                                                                                             PRINTS; PR00438;
                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                           PIR;
                                                                                                                                                                                                                                                                                                                                                                               "Luteinizing hormone of the sperm whale. Amino acid reduced and carboxymethylated beta-subunits.";
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-84281133;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Physeteridae; Ph
NCBI_TaxID=9755;
                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                Pankov Y.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUTROPIN BETA CHAIN (LUTEINIZING HORMONE BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                  THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS. SUBUNIT: HETEROIDINER OF A COMMON ALPHA CHAIN CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
                                                                                                                                                                                                                                                        SIMILARITY: BELONGS FAMILY.
                                                                                                                                                                                                                       PN0141; PN0141. ; P01233; 1HRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLGP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGRPPHHPYDTKDVSEYSCRELHYTRFVTDGPCRSAKPVTELVCSGQCGPARLLPNAIGR 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKWWRPNGPDFRCIPDRYRAQRVQLL-CPGGAAPRSRKVRLVASCKCKRLTRFHNQSELK
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6lycoprotein.

9 57

23 72

26 110

34 88

38 90

3 93 100
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                                                                                                         00007; Cys_knot; 1.
PRO0438; GFCYSKNOT.
PS00261; GLYCO_HORMONE_BETA_1;
PS00689; GLYCO_HORMONE_BETA_2;
                                                                                                                                                                         : IPR000359; -. : : IPR001545; -. : : IPR002400; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22, Created)22, Last sequence update)40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=6466737;
sev V.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139
52
16285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sperm whale luteinizing Res. 28:124-129(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .48;
                                                                                                                                                                                                                                                                     TO THE GLYCOPROTEIN
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Pred.
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N-LINKED (GLCNAC. . .) (POTENTIAL).

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C SIMILARITY.
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No. 0
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                                                                                                                                                                                                                                                                                                                                               AND OVULATION
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                                                                                                                                                                                                                                                                     HORMONES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hormone.";
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                                                                                                                                                                                                                                                                                                   AND A UNIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                     BETA CHAIN
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                                                                                                                                                                                                                                                                                                                                                 STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
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                                                                                                                                                                                                                                                                                                                  BETA
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В
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                  InterPro: IPR000359; ...
InterPro: IPR001545; ...
Pfam; PE00007; Cys_knot; 1.
PROSITE; PS00681; GLYCO_HORMONE_BETA_1;
PROSITE; PS00689; GLYCO_HORMONE_BETA_2;
                                                                                                                                                                      modified
entities
or send a
                                                                                                                                                                                                                                                   This SWI
between
              PROSITE; Hormone;
                                                                                                                        EMBL;
                                                                                                                                                                                                                      use
                                                                                                           HSSP; P01233; 1HRP
                                                                                                                                                                                                                                    the
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AF017448; AF090388;

AAC96019. AAC63526.

.1; 1;

Signal;

Glycoprotein 22

SIMILARITY

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Matches
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O46482;
01-OCT-2000 (R
01-OCT-2000 (R
01-OCT-2000 (R
LUTROPIN BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                              "cDNA cloning of luteinizing
                                                                                                                                                                Lawrence S.B., McNatty K.P., Fidler A.E.; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY
                                                                                                                                                                                                                                                                                             TISSUE=Pituitary;
MEDLINE=98345424; PubMed=9680384;
Harrison G.A., Deane E.M., Copper
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9337;
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Ch
Mammalia; Metatheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                Trichosurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BHJ
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                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                    SIMILARITY:
                                                                                                  THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THY
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RP —
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRPINATLAAQNZACPVCITFTTSICAGYCPSMVRVLPAAL-----PPVPZPVCTYRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 29.5
36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197
                                                                                                                                                                                                                                                                                                                                                                                              vulpecula (Brush-tailed possum).
Metazoa; Chordata; Craniata; Vertebrata;
detatheria; Diprotodontia; Phalangeridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
TA CHAIN PRECURSOR (LUTEINIZING HORMONE
                                                                                                                                                                                                                                                   9:638-642(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                   BELONGS TO THE GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
12412
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                                                                                                                                                                                                                                                                                                  Cooper D.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 88;
Pred. No.
                                                                                                                                                                                                                                                                                 hormone subunits
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                    HORMONES BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55;
                                                                                                                                                                                                                                                                                 from brushtail possum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                   THYROTROPIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BETA SUBUNIT) (LSH-
                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi; Trichosurus.
                                                                                                                                   A UNIQUE
                                                                                                                                                                    STIMULATING
                                    ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                   collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138
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Run
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                                                                                                                                                                                                           Result
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  9
110
111
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114
115
116
118
                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
DB
                                                                                                                                                                                                 Score
                                                                                                                                                                               256
96
93.59
92
92
90.5
88
87
87
86.5
87
88
85.5
83
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seq length:
                                                                                                                                                                                                                                                                                       SPTREMBL_16:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb
6: sp_mammal:*
5: sp_mhc:*
7: sp_mhc:*
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3 Q9PWB0
3 Q9PUK2
1 Q9JKW7
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Compugen Ltd
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Ojnyz3 homo sapien
Ojuem9 homo sapien
Ojh772 homo sapien
O73755 gallus gall
O88995 mus musculu
O97867 sus scrofa
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Q9pwb0 gallus gall
Q9puk2 gallus gall
Q9jkw7 mus musculu
                                                Q9wtw6 mus musculu
Q9r0b6 mus musculu
Q95376 homo sapien
                             Q9f4j0 porphyromon
Q9hbz6 homo sapien
070368 rattus norv
088273 mus musculu
Q9r255 mus musculu
                                                          musculu
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Q9ful2 oryza sativ	toxoplasma	Q9fsq3 oryza sativ	homo sapien	homo sapien	bos taurus	human immun	xenopus lae	mus musculu	rattus norv	mus musculu	plasmodium	plasmodium	neurospora	Q9z1k6 mus musculu	054511 yersinia en	Q9xe24 oryza sativ	rattus norv	chironomus	homo sapien	beta vulgar	yersinia pe	homo sapien	homo sapien	drosophila	homo sapien

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Best Local Similarity 41.9
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AL050024; CAB43243.1; -.

InterPro: IPR000359; --

PROSITE; PS01225; CTCK_2; 1.

Hypothetical protein.

NON_TER
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-BRAIN;
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122 RKRA
                                                                                196 RPRA 199
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                                                                                                                                                                                                                                                                                                                  3 CRELRSTKYISDGQCTSISPLKELVCAGECLLLPVLPNWIGGGYGTKYWSRRSSQEWRCV
                                                                                                                                                                                                       PDRYRAQRVQLLCPGGAAPRSRKVRLVASCKCKRLTRFHNQSELKDFGPETARPQKGRKP 195
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Pred. No. 1.8e-18;
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                 Roddiguez Esteban C., Capdevila J., Ec
Ortiz A., Izpisua Belmonte J.C.;
"Caronte, a novel cer-like protein, me
embryonic left-right asymmetry.";
Nature 0:0-0(1999).
EMBL; AF179484; AAD55581.1; -.
InterPro; IPR000359; -.
InterPro; IPR000359; -.; 1.
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O9PWB0;
O1-MAY-2000 (TrEMBLrel. 1
O1-MAY-2000 (TrEMBLrel. 1
O1-MAR-2001 (TrEMBLrel. 1
CERBERUS HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                              Q9PUK2;
Q9PUK2;
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Q1-MAY-2000
Q1-MAR-2001
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Curr. Bi
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MEDLINE=99439862; PubMed=10508582;
Zhu L., Marvin M.J., Gardiner A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Gallus gallus (Chicken).
Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                              Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                    Eukaryota;
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PROSITE; PS01225; CTCK_2; 1.
  PROSITE;
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AF139721;
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PS01225; CTCK_2;
                                                                                                                                                                                                                                                                                                                  Metazoa;
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) (TrEMBLrel. 13,
l (TrEMBLrel. 16,
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31224 MW;
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nes; Phasianidae; Phasianinae;
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                                                                                                                                                                                    A.N.,
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Best Local S
Matches 48
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Best Local
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) CYSTEINE-RICH PROTEIN NEX-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9JKW7 PRELIMINARY;
Q9JKW7;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location and Developmental Expression. Submitted (JAN-2000) to the EMBL/GenBa EMBL; AF223576; AAF34700.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arlotta P., Jenkins N.A., Jay G., Ono S.J., "Isolation of a Full-Length Murine NFX-1 cD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00041; CT; SEQUENCE 272 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000967; -. InterPro; IPR001374; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                            193
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                                                                                                                                                            RKP-----RPRARGAKANQAEL
                                                                                                                                                                                                                                                    C-IPDRYRAQRVQLLCPGGAAPRSRKVRLVASCKCKRLTRFHNQSELKDFGPETARPQKG
                                                                                                                                                                                                                                                                                                                                                                                        LQNQPWQKARNEKHQNRNKKAQGLSEQTSDTSSLE---SVARSESGTNPREHSPSESE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPPQELEN ---- NQTMNRAENGGRPPHHPYDTKDVSEYSCRELHYTRFVTDGPCRSAKPV 100
                                                                                                               RNPPKQESQRHINAGPKTNMSPI
                                                                                                                                                                                                                                                                                                                                           SEYSCRELHYTREVTDGPCRSAKPVTELVCSGQCGPARLLPNAIGRVK--WWRPNGPDFR
                                                                                                                                                                                                         DEIPDPWRFPTLTLQIASCRKP-----
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48; Conservative
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                                                                                                                                                                                                                                                                                                 --KEVVIADPRGAKPKKAAQLTYNYGRG---PKAKGRLRSEWGNRMSPKSE
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31201
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Pred. No. 0.1;
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 93.5; D
Pred. No. 0.5;
26; Mismatches
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                                                                                                                                                            209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Q9Y557

PRELIMINARY;

PRT;

712

AA

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
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1: /SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
2: /SIDSB/gcgdata/geneseg/geneseqp/AA1982.DAT:*
3: /SIDSB/gcgdata/geneseg/geneseqp/AA1982.DAT:*
4: /SIDSB/gcgdata/geneseg/geneseqp/AA1983.DAT:*
5: /SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*
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Gapop 10.0 , Gapext 0.5
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1167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
/SIDSB/gcgdata/genescq/genescqp/AA1190.DAT:*
/SIDSB/gcgdata/genescq/genescqp/AA1191.DAT:*
/SIDSB/gcgdata/genescq/genescqp/AA1991.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11	10	9	8	7	6	5	4	ω	2	1	Result
343.5	861.5	955	1040	1041	1050	1050	1050	1073	1094	1167	Score
29.4	73.8	81.8	89.1	89.2	90.0	90.0	90.0	91.9	93.7	100.0	% Query Match Length DB
206	176	367	213	213	213	213	213	213	211	213	ength I
21	21	21	21	21	22	21	21	21	21	21	æ
AAY75981	AAY96434	AAB26105	AAY96430	AAY96436	AAY97589	AAY96429	AAB26106	AAY96431	AAY96432	AAY96433	ID
Murine skin cell p	Bovine TGF-beta bi	Human DAN/Cerberus	Human TGF-beta bin	Human TGF-beta bin	Human secreted pro	Human TGF-beta bin	Human DAN/Cerberus	Vervet TGF-beta bi	Murine TGF-beta bi	Rat TGF-beta bindi	Description

	45	44	43	42	41	40	39	38	37	36	ω 5	34	ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
	82.5	82.5	82.5	82.5	83	83	83.5	83.5	83.5	83.5	84.5	85.5	85.5	86	86	86	86	86.5	87	88	92	94.5	98.5	98.5	115	115	201	340	340	340	340	343.5	343.5	343.5
	7.1	7.1							7.2						-				7.5						•	9.9				29.1	•		29.4	29.4
	184	184	184	145	474	168	204	158	145	145	229	176	145	938	925	922	921	165	184	168	712	252	102	102	116	116	50	206	206	206	206	206	206	206
	21	20	19	12	22	21	20	20											19			21	21	20	18	18	20	21	20	19	18	22	22	21
AT TOMBENDO	AAY95961	AAY42173	AAW69293		AAB31245	AAY51132	AAY43275	AAY43266	AAY87479	AAR15125	AAP82071	AAY57315	AAR15109	AAY34392	AAY34520	AAY34521	AAY34522	AAW99515	AAW29727	AAY84014	AAB43147	AAY57316	AAB10277	AAY03225	AAW44090	AAW27654	0	AAB10233	AAW95711	AAW58704	AAW09408	AAB55970	AAB55920	AAY76031
	Human gremlin. Ho	Mouse DRM protein	Human b57 protein	hCG/bLH chimera, D	Amino acid sequenc	e cerebra		Human chorionic go	Human chorionic go	hCG/hLH chimera, A	рвое1743-2-9-8 in	Human betahCG/beta	hCG/eLH chimera, E				Porphorymonas ging	horm	DAN and b57 protei	Amino acid sequenc	ORFX OR	-mati			Human secreted pro	ein	5' EST	n adult r	sapiens	small	n smal	cell	ell protein	Murine skin cell p

ALIGNMENTS

RESULT

12-SEP-2000 (first entry)

AAY96433;

AAY96433 standard; Protein; 213 AA

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Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures
                                          WPI; 2000-412321/35.
N-PSDB; AAA29059.
                                                                       Brunkow ME, Galas DJ,
Van Ness J, Winkler DG;
                                                                                                                                                                                                                                 osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization.
                                                                                                                             27-NOV-1998;
                                                                                                                                                24-NOV-1999;
                                                                                                                                                                      08-JUN-2000.
                                                                                                                                                                                          WO200032773-A1.
                                                                                                                                                                                                              Rattus norvegicus.
                                                                                                                                                                                                                                                                Rat TGF-beta binding protein (BEER).
                                                                                                        (DARW-) DARWIN DISCOVERY LTD.
                                                                                                                             98US-0110283.
                                                                                                                                                   99WO-US27990.
                                                                                   Kovacevich B,
                                                                                   Mulligan JT,
                                                                                   Paeper BW;
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RESULT
AAY96432
ID AAY9
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AC AAY9
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AC AAY9
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AT 12-5
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                                                                                                                                                                                                                                                                    osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization.
                                                                                                                                                                                                                                                                                                                                             12-SEP-2000
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                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                     AAY96432 standard; Protein; 211 AA
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                                           Brunkow ME,
Van Ness J,
                                                                                                                     27-NOV-1998;
                                                                                                                                                  24-NOV-1999;
                                                                                                                                                                               08-JUN-2000
                                                                                                                                                                                                             WO200032773-A1
                                                                                                                                                                                                                                                                                                              Murine TGF-beta binding protein (BEER)
N-PSDB; AAA29058
              WPI; 2000-412321/35
                                                                                        (DARW-) DARWIN DISCOVERY LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 100.0%; Score 1167; DB 21; Local Similarity 100.0%; Pred. No. 6.7e-102; hes 213; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                   therapy;
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                                           Galas DJ,
Winkler DG
                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                   98US-0110283
                                                                                                                                                  99WO-US27990
                                                         Kovacevich B,
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                                                         Mulligan
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Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures
                                                                                                                            Claim 5; Page 124; 162pp; English.
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This shows a murine transforming growth factor-beta (TGF-beta) binding protein designated mBEER. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patients own production of BEER polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for aliagnostic assays and for functional studies. BEER may be used to raise antibodies and for identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such as osteopenia, osteoporosis, fractures and other disorders associated with low mineral content.

Sequence 211 AA;

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Best Local Similarity
 Brunkow ME,
                   (DARW-) DARWIN DISCOVERY LTD
                                                                              08-JUN-2000
                                                                                                  WO200032773-A1
                                                                                                                    Cercopithecus pygerythrus
                                                                                                                                       osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization.
                                                                                                                                                                    Vervet TGF-beta binding protein (BEER)
                                                                                                                                                                                        12-SEP-2000
                                                                                                                                                                                                            AAY96431;
                                                                                                                                                                                                                               AAY96431 standard;
                                      27-NOV-1998;
                                                          24-NOV-1999;
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 Galas DJ,
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                                        98US-0110283
                                                          99WO-US27990
                                                                                                                                                                                                                                Protein;
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 Kovacevich B,
                                                                                                                                                                                                                                213
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Pred. No. 4.7e-95;
3; Mismatches 8;
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 Mulligan JT,
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Minimum DB
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Perfect score:
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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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Sequence 159, App Sequence 286, App Sequence 2, App Sequence 3, App Sequence 4, App Sequence 4, App Sequence 9, App Sequence 9, App Sequence 1, App Sequence 6, App Sequence 6, App Sequence 6, App Sequence 3, App Sequence 4, App Sequence 4, App Sequence 3, App Sequence 4, App Sequence 4
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                   RESULT 2
US-09-188-930-286
US-09-188-930-286
Sequence 286, Application US/09188930A
Patent No. 6150502
     GENERAL INFORMATION:
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Qу	Оу Дъ	Qу ДЪ	Qy Db		US E		
174	118	55	6 1	Query Ma Best Loc Matches	RESULT 1 US-09-188-930-159 Sequence 159, Application US/09 Patent No. 6150502 GENERAL INFORMATION: APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Strachan, Lorna APPLICANT: Onrust, Rene APPLICANT: Onrust, Rene APPLICANT: Murison, James Greg APPLICANTON UNMBER: US CURRENT APPLICATION UNMBER: US CURRENT FILING DATE: 1998-11-0 NUMBER OF SEQ ID NOS: 348 SOOTWARE: FastSEQ for Windows SEQ ID NO 159 LENGTH: 206 TYPE: PRT ORGANISM: mouse US-09-188-930-159		228 229 310 321 332 333 334 337 337 344 441 441 441 441 441 441 441
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(DE)	RVKWW- : GTKYWS	NGGRPPHHP- NGGRHFSS	F-CF	(la:	159, Appli 615052, Appli 615052, Appli Fi GATTON Fi Watson, Fi Stracker Fi Murisor INVENTION INV		$\circ \circ $
SVS	SWY 	TG	ACI -:	larity Conserv	DON:		66666677777778888
HNQSELKDFGPETARPQKGRKPRPRA : : ; HNESSHNFESVSPAKPAQHHRERKRA	-RVKWW-RPNGPDFRCIPDRYRAQRVQLLCPGGAAF : : :: : : : :: YGTKYWSRRSSQEWRCVNDKTRTQRIQLQCQDGST-	HHPYDTKDVSEYSCRELHYTRFVTDGPCRS 	MQLSLAPCLACLLYHAAFYAVESQGWQAFKNDATEIIPGLREYPE : : :	y	ati Jam , I , Ma Ren Ja OO OO OO OO OO OO OO OO		
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	RSRKVRLVASCKCKRLT : : : : RTYKITVVTACKCKRYT	PAR PLP	STL 	21;			Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence
	RPNGPDERGIPDRYRAQRVQLLCPGGAAPRSRKVRLVASCKCKRLTRF : :: : : : : : : : : RRSSQEWRCVNDKTRTQRIQLQCQDGST-RTYKITVVTACKCKRYIRQ	YDTKDVSEYSCRELHYTRFVTDGPCRSAKPVTELVCSGQCGPARLLP 	PPQELENNQTMNRAE : : PAHP-SSNSTLNQAR				
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US-08-468-847B-2
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08468847B Patent No. 5780263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
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                NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NGGRPPHHP---YDTKDVSEYSCRELHYTRFVTDGPCRSAKPVTELVCSGQCGPARLLPN 117
                                                                                                 FILING DATE:
                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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Pred. No. 1.4e-28;
2; Mismatches 72;
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Best Local Similarity 39...
"""trhes 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/08468847B Patent No. 5780263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                              INFORMATION FOR SEQ ID NO:
                                                                                REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                       SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      FILING DATE: 6 June CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: MULLINS, J.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 W-RPNGPDFRCIPDRYRAQRVQLLCPGGAAPRSRKVRLVASCKCKRLTRFHNQSELKDFG 183
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                                                TELEPHONE: 201-994-1744
                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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COMPUTER: IE
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                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 LACILMKSCL------AFKNDATEILYSHVVKPVPAHP-SSNSTLNQARNGGRHFSN 62
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                                                                                                                                    REGISTRATION NUMBER:
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TYPE:
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            ENGTH:
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: NEW JERSEY
AMINO ACID
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                206 AMINO ACIDS
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Pred. No. 3.4e-28;
33; Mismatches 70
                                                                                                                    325800-442
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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I51373
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                                                                                                                                                               T18397
A35281
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PN0139
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B36665
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247.083 Million cell updates/sec
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             hypothetical protetonB protein - Ent UZ snRwp protein A Oct-binding factor beta-gonadotropin hypothetical protehypothetical protehypotheti
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choriogonadotropin
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45	44	43	42	41	40	39	38	37	36	ω G	34	ω	32	31	30
70	70	70	70.5	70.5	70.5	71	71	71.5	71.5	71.5	71.5	71.5	71.5	71.5	71.5
7.2	7.2	7.2	7.3	7.3	7.3	7.3	7.3	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4
178	178	129	1496	1134	699	540	119	3570	2148	1736	1497	724	450	342	165
Ν	N	Ν		1	N	N	N	Ν	N	N	N	N	N	ν	
A47291	I51824	T47958	CGHU2V	JN0711	T09069	T47858	A61465	T45025	A56011	T00391	149607	A48569	149481	JC7110	KTHUB
probable finger pr	tumor-suppressive	hypothetical prote	collagen alpha 2(V	protein-tyrosine k	probable cAMP-resp	hypothetical prote	lutropin beta chai	mucin MUC5B, trach	transcription fact	hypothetical prote	procollagen type V	antigen Em100 - Ei	alpha-2 adrenergic	brain-specific mem	choriogonadotropin

ALIGNMENTS

RESULT 2 151373 1uteinizing hormone beta subunit - turkey C:Species: Meleagris gallopavo (common turkey) C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999 C:Accession: 151373 R:You, S:; Foster, L.K.; Silsby, J.L.; el Halawani, M.E.; Foster, D.N. J. Mol. Endocrinol. 14, 117-129, 1995 A:Title: Sequence analysis of the turkey LH beta subunit and its regulation by gonado A:Tetle: Sequence number: 151373; MUID:95290073 A:Accession: 151373 A:Accession: 151373 A:Status: preliminary: translated from GB/EMBL/DDBJ A:Residues: 1-159 < YOU> A:Rolecule type: mRNA A:Residues: 1-159 < YOU> A:Cross-references: GB:L35519; NID:g530952; PIDN:AAA74125.1; PID:g530953 A:Gene: LH-beta	Qy 105 PDRYRAQRVQLLCPGGAAPRARKVRLVASCKCKRLTRFHNQSELKDFGPEAARPQTGRKL 164 ;	Query Match 27.7%; Score 267.5; DB 2; Length 134; Best Local Similarity 43.5%; Pred. No. 1.4e-17; Matches 57; Conservative 23; Mismatches 44; Indels 7; Gaps 4; Matches 57; Conservative 23; Mismatches 44; Indels 7; Gaps 4; Qy 49 CRELHETRYVTDGPCRSAKPVTELVCSGQCGPARLLPNAIGRGKWW-RPSGPDFRCI 104 [A; Reletice number: 2.047.1 A; Accession: TO8710 A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-134 <wan> A; Cross-references: EMBL: AL050024 A; Experimental source: fetal brain; clone DKFZp564D206 C; Genetics: A; Note: DKFZp564D206.1</wan>	T08710 hypothetical protein DKFZp564D206.1 - human (fragment) C;Species: Homo sapiens (man) C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999 C;Accession: T08710 R;Wambutt, R; Heubner, D; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, March 1999

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hypothetical protein F40E10.4 - Caenorhabditis elegans (fragment) C;Speciaes: Caenorhabditis elegans (c;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T22025 R;Smye, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Noce, T.; Ando, H.; Ueda, T.; Kubokawa, K.; Higashinakagawa, T.; Ishii, S. J. Mol. Endocrinol. 3, 129-137, 1989
A;Title: Molecular cloning and nucleotide sequence analysis of the putative cDNA for the A;Reference number: A61091; MUID:89374710
A;Accession: A61091
                                                       submitted to the EMBL Data Library, A;Reference number: Z19503 A;Accession: T22025 A;Status: preliminary; translated fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: pituitary glycoprotein hormone beta chain C;Keywords: glycoprotein; hormone; pituitary F:1-39/Dnmain: slgnal sequence #status predicted <SIG>F:48-73,62-96,65-127,77-149,111-139,129-132/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-158 <NOC>
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                    A; Molecule type: DNA
A; Residues: 1-601 <WIL>
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A;Cross-references: EMBL:Z69792; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F40E10.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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Aternate names: luteinizing hormone beta chain
species: Gallus gallus (chicken)
;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 GGRPP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKWWRPSG--PDFRCIPDRYRAQRVQLL-CPGGAAPRARKVRLVASCKCKRLTRFHNQSE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPLGRP--PQSSCTYGALRYERWALWGCPIGSDPRV-LLPVALSCRCARCPIATSDCTVQ 142
                                                                                                                                                                                                                                                                                                                                                                                                                        --YRSPLGPPPQSACTYGALRYERWALWGCPIGSDPRV-LLPVALSCRCARCPMATSDCT 140
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26.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 94.5; DB 2;
Pred. No. 0.12;
                                                              from
                                                                                                                        February 1996
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                                                              GB/EMBL/DDBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56;
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DNA repair protein sms - syphilis spirochete

N;Alternate names: DNA repair protein radA
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 19-Jan-2001
C;Accession: A71251
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          luteinizing hormone beta-subunit - quail
C;Species: Coturnix coturnix (quail)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: I51242
R;Ando, H; Ishii, S.
Gen. Comp. Endocrinol. 93, 357-368, 1994
A;Title: Molecular cloning of complementary deoxyribonucleic acids for the particle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-166 <AND>
A;Residues: 1-165 <AND>
C;Superfamily: pituitary glycoprotein hormone beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 urnix coturnix japonica).
A;Reference number: I51241; MUID:94252550
A;Accession: I51242
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Map position: X
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                      A; Molecule type: DNA
A; Residues: 1-455 <C
                                                                                                                     A; Title: Complete genome sequence of Treponema A; Reference number: A71250; MUID:98332770
A;Cross-references: GB:AE001270; GB:AE000520; NID:g3323350; PIDN:AAC65973.1; PID:g332
                                                                    A; Status: nucleic acid sequence not shown; translation not
                                                                                           A; Accession: A71251
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Best Local S
Matches 31
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Best Local Similarity
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31; Conservative
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Pred. No. 1.3;
l3; Mismatches
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Pred. No. 1.
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P45646 meleagris g
P45657 coturnix co
O46482 trichosurus
O83985 treponema p
P5330 physeter ca
P24014 drosophila
O43474 homo sapien
P3351 mus musculu
O97012 rattus norv
O97012 rattus norv
O97013 homo sapien
P33684 struthio ca
P46383 enterobacte
Q13421 homo sapien
O77835 ceratcheri
O60793 mus musculu
P07434 papio anubi
P38565 xenopus lae
O44890 drosophila
P56945 homo sapien
O46483 macropus ru
Q16633 homo sapien
O77805 felis silve
P01233 homo sapien
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O66806 mus musculu
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1	This SWISS-PROT entry is copyright. It is produced through a colla between the Swiss Institute of Bioinformatics and the EMBL outs the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for coentities requires a license agreement (See http://www.isb-sib.ch/aor send an email to license@isb-sib.ch).	SEQUENCE FROM N.A. TISSUE=Pituitary; MEDLING=95290073; PubMed=7772235; YOU S., Foster L.K., Silsby J.L., e "Sequence analysis of the turkey LH by gonadotrophin-releasing hormone of the pituitary cells."; J. Mol. Endocrinol. 14:117-129(1995) -: FUNCTION: PROMOTES SPERMATOGENEE THE TESTES AND OVARIES TO SYNTH -: SUBUNIT: HETERODIMER OF A COMMO CHAIN WHICH COMFERS BIOLOGICAL LUTROPIN, FOLLITROPIN AND GONAD -: SIMILARITY: BELONGS TO THE GLYC FAMILY. This SWISS-PROT entry is copyright. between the Swiss Institute of Bio the European Bioinformatics Institut use by non-profit institutions a modified and this statement is not entities requires a license agreeme or send an email to licensee agreeme or send an email to licensee agreeme

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PROSITE; PS00261; GLYCO_HORMONE_BETA_1;
PROSITE; PS00689; GLYCO_HORMONE_BETA_2;
                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning of complementary deoxyribonucleic acids for the pituitary glycoprotein hormone alpha-subunit and luteinizing hormo beta-subunit precursor molecules of Japanese quail (Coturnix cotur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HO
BETA) (LSH-B) (LH-B).
                                                                                                InterPro; IPR000359;
InterPro; IPR001545;
InterPro; IPR002400;
                                                                                                                                                    EMBL; S70834; AAB30867.1;
HSSP; P01233; 1HRP.
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                  Hormone; Signal;
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                                                                                                                                                                                                                                                                                                                                             LUTROPIN, FO SIMILARITY: FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                         Comp. Endocrinol. 93:357-368(1994).

FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.

SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H., Ishii S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLGP 146
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Y: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
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 Glycoprotein.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

LAWYENCE S.B., MCNATTY K.P., Fidler A.E.;

Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.

1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.

1- TMITARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Pituitary;
MEDLINE=98345424; PubMed=9680384;
Harrison G.A., Deane E.M., Cooper D.W.;
"cDMA cloning of luteinizing hormone su
and red kangaroo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trichosurus vulpecula (Brush-tailed possum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 GRPPHHPFETKDASEYSCRELHFTRYVTDGPCRSAKPYTELVCSGQCGPARLLPNAIGRG
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BETA CHAIN PRECURSOR (LUTEINIZING HO
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Pred. No. 0.29
L3; Mismatches
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1: sp_archea:*
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5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:
11: sp_rodent:
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Comp
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Q9x1k6 mus musculu
Q9v7f8 drosophila
Q9xyv4 drosophila
Q9v7f9 drosophila
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Q9puk2 gallus gall
Q9y557 homo sapien
Q9nyz3 homo sapien
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073755 gallus gall
097867 sus scrofa
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7.7	7.7	7.7	7.7	7.7	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.9	7.9							8.1	8.2
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₩.	070368 rattus norv	Q9ubcl homo sapien		Q9h611 homo sapien		Q25757 plasmodium	Q9xsv8 bos taurus	Q9psh2 gallus gall		Q9ujd7 homo sapien	095813 homo sapien	homo	Q9r255 mus musculu	Q9ubx4 homo sapien	Q52730 rhizobium e	Q94446 chironomus	Q9qw33 rattus sp.	homo	Q14859 homo sapien	homo	homo	070326 mus musculu	035793 rattus norv	₽	Q9unp3 homo sapien

ALIGNMENTS

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Best Local Similarity
Matches 57; Conserv
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O993U3;
O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHEFICAL 15.3 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                       TISSUE-BRAIN;
Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL050024; CAB43243.1; -.
Interpro; IPR000359; -.
Interpro; IPR000359; -.
PROSITE; PS01225; CTCK_2; 1.
                                                                                                                                                                                                                                                      Hypothetical protein.
NON_TER 1
SEQUENCE 134 AA; 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKF2P564D206.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
120 RERKRASKSSK 130
                             165
                                                                                      105
                                                          63
                                                                                                                                     49 CRELHFTRYYTDGPCRSAKPYTELYCSGQCGPARLLPNAIGRG---KWW-RPSGPDFRCI 104
                                                                                                                    3 CRELRSTKYISDGQCTSISPLKELVCAGECLLLPVLPNWIGGGYGTKYWSRRSSQEWRCV 62
                                                                         NDKTRTQRIQLQCQDGST-RTYKITVVTACKCKRYTRQHNESSHNFESMSPAKPV--QHH 119
                           RPRARGTKASR 175
                                                                                                                                                                                                                                                        134 AA; 15324 MW; A0B7A8650D2EE6F1 CRC64;
                                                                                                                                                                               Conservative
                                                                                                                                                                             27.7%; Score 267.5; DB 4; 43.5%; Pred. No. 3.8e-20; tive 23; Mismatches 44;
                                                                                                                                                                                                          Length 134;
                                                                                                                                                                             Indels
                                                                                                                                                                               7;
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                                                                                                                                                                             Gaps
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RESULT
Q9PUK2
ID Q0
AC Q0
DT 00
DT 00
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Best Local S
Matches 26
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O9PWB0;
O1PWB0;
O1-MAY-2000 (TIEWBLITE1. 1
O1-MAY-2000 (TIEWBLITE1. 1
O1-MAR-2001 (TIEWBLITE1. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9PUK2;
Q9PUK2;
Q1-MAY-2000
Q1-MAY-2000
Q1-MAR-2001
SMART; SP
SEQUENCE
                                 Interpro; IPR000359; -.
Interpro; IPR001839; -.
Probom; PD000357; -; 1.
PROSITE; PS01225; CTCK_2; 1.
                                                                                                                                                                       Rodriguez Esteban C., Capdevila J., Ortiz A., Izpisua Belmonte J.C.; "Caronte, a novel cer-like protein, embryonic left-right asymmetry.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARONTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SP
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000359; -.
PROSITE; PS01225; CTCK_2; 1.
SMART; SM00041; CT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Archosauria; Aves; Neognathae;
                                                                                                                                 Nature 0:0-0(1999).
EMBL; AF179484; AAD55581.1; -.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; (Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Curr. Biol. 9:931-938(1999).
EMBL; AF139721; AAD51610.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhu L., Marvin M.J.,
Levin M.;
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-99439862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID~9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CERBERUS HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heart."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cerberus regulates left-right
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPDDRLYTFCSKCLPTKFSMKHLDLNCT-SSVPVVKKVMIVEECNCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIKTNEMHQETCRTLPFSQSVAHESCEKV-IVQNNLCFGKCSS-----
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SM00041;
ICE 272 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00041; CT.
CE 272 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TremBLrel. 13, Created)
(TremBLrel. 13, Last sequence u
(TremBLrel. 16, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                CT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=10508582;
J., Gardiner A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.
31224 MW;
31201 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.5%;
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16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 102; DB 1
Pred. No. 0.009;
                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
  0D89729715771BC2
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                                                                                                                                                                                                                                            Economides A.N., Pascual J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272
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on update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stern C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97
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RESULT CONTROL OF CONT
   QUITES OF THE PROPERTY OF THE 
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Best Local S
Matches 34
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Best Local
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01-OCT-2000
01-OCT-2000
01-OCT-2000
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DJ1163J1.3 (NOVEL PROTEIN SIMILAR TO MOUSE 899) (1
                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Monte M., Collavin L., Lazarevic D., Utrera

"Cloning, chromosome mapping and functional

"Cloning, chromosome mapping applications of murine B99.";
"Cloning, chromosome mapping and functional ch
human homolog gene of murine B99.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
EMBL; AF223408; AAF31459.1; -
SEQUENCE 720 AA; 76628 MW; D4E852CE4BE85BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-1999) to the EMBL; AL031588; CAB38415.1; NON_TER 1
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DJ1163J1 3.

Homo sapiens (Human).

Tharvota; Metazoa; Chordata;

Tharvota; Primates;
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9NYZ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 PANSSRPLSNISKSGRMGPAMLRPALPAGPVGASSW-------QAKRVDVSE 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPDFR-----CIPDRYRAQRVQLLCPGGAAPRARKVRLVASCKCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----QLLCPGGAAP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPTNQFKIPKFSIGDSPDSSTPKLSRAQRPQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFHNQSELKDF----GPEAARPQTGRKLRPRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIKTNEMHQETCRTLPFSQSVAHESCEKV-IVQNNLCFGKCSS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFETKDASEYSCRELHFTRYVTDGPCRSAKPVTELVCSGQCGPARLLPNAIGRGKWWRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              0 (TrEMBLrel. 15, 0 (TrEMBLrel. 15, 0 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         712 AA;
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Primates;
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Pred. No. 0.014;
7; Mismatches 42;
                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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1: /SIDSB/gcgdata,

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Gapop 10.0 , Gapext 0.5
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967
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                  AAB26106
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132.908 Million cell updates/sec
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                                   Human TGF-beta bin
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Rat TGF-beta bindi
Murine TGF-beta bi
                                                                                                                                                                                                                                  Description
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Vervet TGF-beta bi
Human DAN/Cerberus
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	ein (BEER).	prot	inding	TGF-beta binding protein	Bovine TGF	Во
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					AAY96434;	AA
	176 AA.	in;	; Protein;	tandard;	96434 s	AA)
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	ALIGNMENTS					
	AAY42172	20	184		77.5	45
(†	AAW27680	18	145		77.5	44
hCG/eLH chimera, E	AAR15109	12	145	æ æ ⊙ ⊢	77.5	4 4
Disease associated	AAW88432	20	685		79	1
serum	AAY00915	20	685	8.2	79	40
Human RKLF protein	AAB13774	21	479		79	39
GKLF prot	AAB48018	22	470		79	37
RKLF prot	AAB13773	21	470			36
	AAY24314	20	470		79	35
Herpes simplex vir	AAY78333	21	246	8 C	79	ω L 4
Drosophila SLIT pr	AAR25079	20	1480		79.5 79	υ Ω Ω υ
	AAY43278	20	212		80.5	31
hCG/eLH chimera, E	AAR15113	12	145	ထဖ ဟ တ	82.5	30
DAN and b57 protei	AAW29727	19	184		3 85	28
	AAY04748	20	320		85.5	27
Murine cerebral ne	AAY51132	21	168		86°	26
ORE	AAB43147	2 22	712	9.6	93	2 л. 4
	AAY12009	20	50		96	23
Human fetal kidney	AAB10277	21	102	0:	103.5	22
secre	AAW44090	20	116	10.2	103.5	20
ted prote	AAW27654	8 2	116	٠,-	108.5	19
Human adult retina	\sim	21	206	4.	333	18
	AAW95711	20	206		ω (ω (17
Human small CCN-li	AAW09408	1 6	206	34.4 4	ىنا ئىد ئىيا ئىد ئىيا ئىد	א מ
cell pr	AAB55970		206	4	336	14
ell protein	559	22	206	34.7	336	3
Murine skin cell p	AAY76031		206	4	336	12

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PPI
                                                                                                                                                         osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization.
                          N-PSDB;
                                   WPI; 2000-412321/35.
                                              Brunkow ME, Galas DJ,
Van Ness J, Winkler D
                                                                                                                08-JUN-2000.
                                                                                                                              WO200032773-A1
                                                                                                                                              Bos taurus.
                                                                     (DARW-) DARWIN DISCOVERY LTD
                                                                                    27-NOV-1998;
                                                                                                  24-NOV-1999;
                            AAA29060
                                                                                    98US-0110283
                                                                                                   99WO-US27990
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                                                        Kovacevich B,
                                                        Mulligan JT,
                                                        Paeper BW;
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Human DAN/Cerberus Murine skin cell p

Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteopensis and fractures

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RESULT
AAY96431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patients own production of BEER polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for diagnostic assays and for functional studies. BEER may be used to raise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This shows a bovine transforming growth factor beta (TGF-beta) binding protein designated bBEER. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or
Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures
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                                                                                                                                                                                                                                           Brunkow
                                                                                                                                                                                                                                                                                                                                                                                                                  24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecus pygerythrus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteopathic; transforming growth factor-beta; TGF-beta; binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vervet TGF-beta binding protein (BEER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-2000
                                                                                                                                                                                                                                                                                               (DARW-) DARWIN DISCOVERY LTD
                                                                                                                                                                                                                                                                                                                                                             27-NOV-1998;
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                                                                                                                     2000-412321/35
DB; AAA29057.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy;
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Winkler D
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                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US27990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antisense therapy; fracture; bone mineralization
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Pred. No. 1.5e-87;
); Mismatches 0;
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                                                                                                                                                                                                                                           Mulligan JT,
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                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patients own production of BEER polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for diagnostic assays and for functional studies. BEER may be used to raise antibodies and for identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such as osteopenia, osteoporosis, fractures and other disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This shows a vervet transforming growth factor beta (TGF-beta) binding protein designated vBEER. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 122-123; 162pp; English
                                                                                                                                                                 02-MAR-2000; 2000WO-US05537
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                          AAB26106
                                                                                                                                                                                                                                                                                                                                                                                                   AAB26106 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              associated with low mineral content.
                                                N-PSDB;
                                                                                                               (REGE-)
                                                                                                                                                                                           21-SEP-2000
                                                                                                                                                                                                                    WO200055193-A2
                                                                                                                                                                                                                                                                                  antagonist;
                                                                                                                                                                                                                                                                                                Human; DNA/Cerberus-related protein 6; hDCR6; morphogenic protein;
                                                                                                                                                                                                                                                                                                                       Human DAN/Cerberus-related
                                                                                                                                                                                                                                                                                                                                                 15-JAN-2001
                                                                                                                                       12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                              2000-638179/61
                                                                                                                                                                                                                                                                    therapy
                                                                                                               REGENERON
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                                                AAA94051
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                                                                                                                                                                                                                                                                                  BMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                          99US-0124118
                                                                                                                                                                                                                                                                                 cell growth;
                                                                                                                PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.2%;
95.5%;
                                                                                                                                                                                                                                                                                                                       protein 6 (hDCR6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                    213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 920.5; DB 2
Pred. No. 7.2e-83;
                                                                                                                                                                                                                                                                                     cell differentiation;
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Novel isolated, human DNA/Cerberus related protein 6 which include natural homologue, and polypeptides comprising DCR6 domain and nucacids encoding the proteins which are useful as probes and primers ${\sf C}$

and nucleic

Title: Perfect score: Sequence:

US-09-668-021-16 967 1 NDATEIIPELGEYPE

NDATEIIPELGEYPEPLPEL...

.....RPQTGRKLRPRARGTKASRA 176

(without alignments)
82.753 Million cell updates/sec Search time 47.86 Seconds

Scoring table:

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on:

OM protein

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protein search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Comp

Compugen Ltd

November 7, 2001, 15:47:18;

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: MISSON, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 159
LENGTH: 206
TYPE: PRT
COLANIEW. TOLSE
                           RESULT 2
US-09-188-930-286
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US-09-188-930-159
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Sequence 286, Application US/09188930A Patent No. 6150502 GENERAL INFORMATION:
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Best Local
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                                                                                     174
                                                                                                        144
                                                                                                                           114 QLLCPGGAAPRARKVRLVASCKCKRLTRFHNQSELKDFGPEAARPQTGRKLRPRARGTKA 173
                                                                                                                                              84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SK
                                                                                     SR 175
                                                                                                        QLQCQDGST-RTYKITVVTACKCKRYTRQHNESSHNFESVSPAKP--AQHHRERKRASKS
                                                                                                                                                       VTDGPCRSAKPVTELVCSGQCGPARLLPNAIGRG---KWW-RPSGPDFRCIPDRYRAQRV 113
                                                                                                                                                                                   NDATEILYSHVVKPVPAHPSSNSTLNQARNGGR--HFSSTGLDRNSRVQVGCRELRSTKY
                                                                                                                                              ISDGQCTSISPLKELVCAGECLPLPVLPNWIGGGYGTKYWSRRSSQEWRCVNDKTRTQRI
                                                                   202
                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.7%;
41.8%;
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US-08-018-288-18
US-08-018-287-474-1
US-08-18-0-991-8
US-08-910-991-8
US-08-910-991-8
US-08-913-821-6
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US-09-282-357-3
US-09-282-357-3
US-09-282-357-3
US-09-282-357-3
US-09-282-357-3
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                                                                                                                                                                                                                                  Score 336; DB 4;
Pred. No. 5.7e-28;
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                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                          65;
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10, Appl
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Result

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analysis of the total score distribution.

SUMMARIES

No

Score

Match

Length

DB

ID

Description

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US-09-188-930-286
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US-08-468-847B-20
US-09-540-245A-9
US-09-540-245A-7
US-09-540-245A-7
US-09-540-245A-7
US-09-540-245A-7
US-09-540-245A-7
US-09-309-053-2
US-08-946-241B-9
US-08-946-241B-9
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US-08-946-241B-9
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US-08-316-282-2
US-09-282-357-24-2
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US-08-426-819A-35
US-08-426-819A-35
US-08-426-819A-35
US-08-215-035-2

Sequence 159, App
Sequence 286, Appli
Sequence 20, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
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1480 1480 1480 1470 470 479 685 685 685 685 685 234 234 234 234

Database

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/Packfiles1.pep:*

Minimum Total number

Maximum

DB DB

seq

length: 0 length: 2000000000

of hits satisfying chosen parameters:

212252 seqs, Gapop 10.0 , BLOSUM62

Gapext 0.5 22503292 residues

Post-processing:

Minimum Match

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

6;

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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Orrust, Rene
APPLICANT: Orrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: And Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 286
LENGTH: 206
TYPE: PRT
ORGANISM: Mouse
US-09-188-930-286
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Best Local 9
                                                                                                                                          COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/46/
ETILING DATE: 6 June 1995
CLASSIFICATION : 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-442
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
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CITY: ROSELAND
STATE: NEW JERSEY
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nes 76; Conserv
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41.8%; Pred. No. 5.7e-28;
ative 29; Mismatches 65; Indels
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US-08-468-847B-20; Sequence 20, App.; Patent No. 5780
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 AMINO ACIDS
                                                                                                                                                                                                                                               SOFTWARE: WORD PERFECT 5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hastings, Gregg A. and Adams, Mark D.
TITLE OF INVENTION: Human CCN-Like Growth Factor
RUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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TYPE: AMINO ACID
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PS,
OPERATING SYSTEM:
                                                                                                                                       NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
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TYPE: AMINO ACID
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                                                                                                                                                                                                                                 APPLICATION NUMBER:
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STRANDEDNESS
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41.8%; Pred. No. 1.2e-27;
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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length: 2000000000
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2301
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EST:*
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gb_est2:*
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em_estom1:
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gb_est55:*
gb_est57:*
gb_est50:*

gb_est41:*
gb_est42:*
gb_est43:*
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1117: gb_est48: *
1119: gb_est50: *
1120: gb_est50: *
1121: gb_est50: *
1122: gb_est50: *
1123: gb_est50: *
1124: gb_est50: *
1125: gb_est50: *
126: gb_est50: *
127: gb_est50: *
128: gb_est50: *
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142: gb_est80: *
143: gb_est810: *
142: gb_est81: *
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144: gb_est81: *
155: gb_est81: *
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Pred. No. is the number of results predicted by chance to has score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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1: /SIDS1/gcgdata,
2: /SIDS1/gcgdata,
3: /SIDS1/gcgdata,
4: /SIDS1/gcgdata,
5: /SIDS1/gcgdata,
6: /SIDS1/gcgdata,
6: /SIDS1/gcgdata,
7: /SIDS1/gcgdata,
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Match Length DB
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SIDS1/gcgdata/geneseq/geneseqn/NA1981.DAT:

SIDS1/gcgdata/geneseq/geneseqn/NA1981.DAT:

SIDS1/gcgdata/geneseq/geneseqn/NA1983.DAT:

SIDS1/gcgdata/geneseq/geneseqn/NA1985.DAT:

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SIDS1/gcgdata/geneseq/geneseqn/NA1995.DAT:

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Human secreted pro Mutant human TGF-b Human TGF-beta bin Human TGF-beta bind Rat TGF-beta bindi Murine TGF-beta bi Bovine TGF-beta bi WPI; 2000-412321/35 Brunkow ME, Van Ness J, 08-JUN-2000. Cercopithecus pygerythrus 27-NOV-1998; 24-NOV-1999; WO200032773-A1. (DARW-) DARWIN DISCOVERY LTD. Galas DJ, Winkler DG; 98US-0110283. 99WO-US27990 Location/Qualifiers
1..642 /*tag= a /product= TGF-beta_binding_protein /*tag= Kovacevich B, Mulligan JT, Paeper BW;

BEER; gene therapy; antisense therapy; fracture; bone mineralization;

SS.

Human DAN/Cerberus

P-PSDB; AAY96431

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibodies and for identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such as osteopenia, osteoperosis, fractures and other disorders associated with low mineral content.
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Matches 624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; DNA/Cerberus-related protein antagonist; BMP; cell growth; cell d gene therapy; ss.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Brunkow, M.E., Gardner, J.C., Van Ness, J., Paeper, B.W., Kovacevich, B.R., Proll, S., Skonier, J.E., Zhao, L., Sabo, P.J. Fu, Y.H., Alisch, R.S., Gillett, L., Colbert, T., Tacconi, P., Hamersma, H., Beighton, P. and Mulligan, J.T.

Bone Dysplasia Sclerosteosis Results from Loss of the SOST Product, a Novel Cystine Knot-Containing Protein Am. J. Hum. Genet. 68 (3), 577-589 (2001)
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                                                                           Submitted (07-DEC-2000) Genomics, 220th St. SE, Bothell, WA 98021, (
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Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,
Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.
Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P., C
Hamersma,H., Beighton,P. and Mulligan,J.T.
Direct Submission
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 2329)
Botstein,D.A., Goddard,A., Gurney,A.L., Smith,V., Wa Wood,W.I.
Compositions and methods for the treatment of tumor patent: WO 0075317-A 19 14-DEC-2000;
Genentech, Inc. (US)
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2307	GAATTAACAGTCTGTTCTTCCAGAGTCCAGAGACATTGTTAATAAAGACAATGAATCATG	2248	рb
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1947	> −	1888	Db
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Submitted (22-DEC-2000) Medical Genet
Universiteitsplein 1, Antwerp B2810,
Location/Qualifiers
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Increased bone density in sclerosteosis is due to the defici a novel secreted protein (SOST)
Hum. Mol. Genet. 10 (5), 537-543 (2001)
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Best Local Similarity 98.9%;
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Submitted (07-DEC-2000) Genomics,
220th St. SE, Bothell, WA 98021, U
Location/Qualifiers
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Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.
Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P., G
Hammersma,H., Beighton,P. and Mulligan,J.T.
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1 (bases 1 to 21501)

Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,

Kovacevich,B.R., Proll,S., Skonier,J.E., 2lao,L., Sabo,P.J.,

Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P., Galas,D.,

Hamersma,H., Beighton,P. and Mulligan,J.T.

Bone Dysplasia Sclerosteosis Results from Loss of the SOST Gene

Product, a Novel Cystine Knot-Containing Protein

Am. J. Hum. Genet. 68 (3), 577-589 (2001)
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LVASCKCKRLTERHNQSEIKDFGTEAARPQKGKKPRPRARSAKANQAELENAY"
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15429		1537	
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                                                                 E 2 (bases 1 to 94752)

8S Birren, B., Fasman, K., McKernan, K., Munro, C., Nusbaum, C.,

8S Birren, B., Fasman, K., McKernan, K., Munro, C., Nusbaum, C.,

8S Birren, B., Fasman, K., McKernan, K., Munro, C., Nusbaum, C.,

8C Birren, B., Fasman, K., Baldwin, J., Barna, N., Cantu, C., Chang, A.,

8C Cooke, P., Daly, M.J., Devon, K., Dewar, K., Durette, B., Forrest, C.,

9C Cooke, P., Daly, M.J., Devon, K., Geraigery, K., Gilmartin, T., Hagos, B.,

9C Gage, D., Gensheimer, S., Geraigery, K., Gilmartin, T., Hagos, B.,

9C Halphen, I., Harris, K., Howland, J.C., Huang, J., Hui, L., Jacotot, L.,

8Kirby, A., Lane, M., MacKenzle, J., Marquis, N., McDermott, J.,

9C Milla, M., Morrow, J., Nachman, A., Naylor, J., O'Connor, T., Olotu, A.,

9C Milla, M., Morrow, J., Nachman, A., Naylor, J., O'Connor, T., Olotu, A.,

9C Milla, M., Morrow, J., Nachman, A., Naylor, J., O'Connor, T., Olotu, A.,

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9C Milla, M., Morrow, J., Nachman, A., Naylor, J., O'Connor, T., Olotu, A.,

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9C Milla, M., Morrow, J., Nachman, A., Maria, M., Naylor, J., O'Connor, T., Olotu, A.,

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9C Milla, M., Morrow, J., Nachman, A., Maria, M., Naylor, J., O'Connor, M.,

9C Milla, M., Morrow, J., Nachman, A., Maria
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     Birren,B.,
Lander,E.,
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AC003098
AC003098.1 GI:2822155
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1 (bases 1 to 94752)
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens chromosome 17, Unpublished 2 (bases 1 to 94752)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Fasman, K., McKernan, K.,
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Fasman,K., McKernan,K., Nusbaum,C., Richardson,P.,
Allen,N., Baker,J., Baldwin,J., Barna,N., Beckerly,R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (29-JAN-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 29, 1998 this sequence version replaced gi:2665504. The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.
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complement(11505. .11804)
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complement(972...1262)
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complement(1884...1912
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complement(12104. .12476)
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11811
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lement(12775. .
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complement(32675. .33003)
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27862 27906
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24329. .2
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20893..2
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26060. .26174
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25805
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/rpt_family="MLTIC"
complement(13544. .13847)
/rpt_family="AllSx"
                                            complement(33042. .33082)
/rpt_family="LINE2"
33363. .33459
                                                                                                                                                                                                                                                            complement(29498. .29
/rpt_family="GC_rich"
30074. .30181
                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="LINE2"
28068. .28114
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25542. .25698
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/rpt_family="LINE2"
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complement(28329.
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22577. .22633
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complement(21495
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18031. .18178
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'4. .1600'
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4. .30249)
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                                                                      gagctcaaggacttcgggaccgaggccgctcggccgcagaagggccggaagccgcgcgccc
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                         GAGACCTTCCAGGCCCTGAGGAATCCCGGGCCGGCAAGGCCCCCCCTCAGCCCGCCAGC
                                     GAGCTCAAGGACTTCGGGACCGAGGGCCGCTCGGCCGCAGAAGGGGCCGGAAGCCGCGGCCC
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 tgaggggtcccacggggcagggagggaattgagagtcacagacactgagccacgcagcc
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/rpt_family="LIMD2"
complement(37477...37777)
/rpt_family="Alusx"
complement(37804...37948)
/rpt_family="L1"
37948...38130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="MLT2D"
35495. .35591
/rpt_family="(GA)n"
complement(35561. .3
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complement(35678, .35935)

/rpt_fam:)
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/rpt_family="MER66B"
complement(36450. .36867)
/rpt_family="MLT2D"
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/rpt_family="Alusg"
complement(36236...36449)
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complement/lena"
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REFERENCE
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TITLE
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                                                                                                                                                                                                                                                                                          Submitted (18-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 22, 2000 this sequence version replaced gi:8920653. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., StangerThomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye, Young,G., Zainoun,J., Zimmer,A. and Zody,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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Birren, B., Linton, L.,
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                                                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                               Web site: http://www-seq.wi.mit.edu
                                                                                                             Center code: WIBR
                                                                                                                                                       Center: Whitehead
          Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                       Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ye,W.J.
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NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap; version 0.960731
Consensus quality: 139835 bases at least Q40
Consensus quality: 145751 bases at least Q30
Consensus quality: 148014 bases at least Q20
Insert size: 155000; agarose-fp
Insert size: 14980; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; agarose-f
Quality coverage: 3.9 in Q20 bases; agarose-f
                                                                                                                                                                                                                                                                                                                                                    26840 : contig of 3743 bp in 1.
26841 26940: gap of 100 bp
26941 32331: contig of 5391 bp in 1e.
32332 32431: gap of 100 bp
32432 37589: contig of 57150
37590 37689: gap of 37690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Summary Statistics
Sequencing vector: M13; M77815; 94% of reads
Sequencing vector: Plasmid; n/a; %-0.f%% of re
6.15883306320908Chemistry: Dye-terminator Big
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name:
                135005 135104: gap of 100 bp
135105 151780: contig of 16676 l
                                                118634 118733: gap of 118734 135004: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1284 1383:
1384 29
2932 3031:
                                                                                                                                                                                                                                                                                                                                                                                                                                        17465: contig of 3656 bp in
167 17566: gap of 100 bp
1877: contig of 3656 bp in
1977: contig of 2181 bp in 1
1848 19847: gap of 100 bp
148 22997: contig of 3150 bp in 1
98 23097: gap of 100 bp
18 26840: contig of 3150 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 8684: gap of 100 bp in 10

25 10824: contig of 2140 bp in 10

25 10924: gap of 100 bp

25 13710: contig of 2786 bp in 10

11 13810: gap of 100 bp

11 17466: contig of 3656 bp in 10
Location/Qualifiers
                                                                                                                                                    100 bp
1472: contig of 8266 bp in
81572: gap of 100 hn
94653
                                                                                106859: gap of
118633: cont
                                                                                                                                    94753:
                                                                                                                                                                                                                                      64003:
                                                                                                                                                                                                                                                                       57082:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6477:
                                                                                                                                                                                                                                                                                          63903: contig of 6821 bp in 16
4003: gap of 100 bp
73106: contig of 9103 bp in 1e
8206: gap of 100 bp
81477:
                                                                                                              100 bp
94653: contig of 13081 bp in length
1753: gap of 100 bp
176759: contig of 12006 bp in length
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2931:
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0982: contig of 7287 bp
1: gap of 100
901:
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                                         ap of 100 bp contig of 16271 b
                                                                           ap of 100 bp contig of 11774 h
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of 2117 bp
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BASE COUNT
ORIGIN
                                                                                                                 Query Match 88.5%;
Best Local Similarity 98.9%;
Matches 2060; Conservative
                                                                    112051 CAGGGGTGGCCAGGGGGGCGCCACCCTCACGCGCGCCTCTCTCCACAGACGTGTCCGAG 112110
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                      tacagctgccgcgagctgcacttcacccgctacgtgaccgatgggccgtgccgcagcgcc 338
                                                                                  cgggcggagaacggagggcggcctccccaccacccctttgagaccaaagacgtgtccgag 278
aagccggtcaccgagctggtgtgctccggccagtgcggcccggcgcgcctgctgcccaac
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26941. .32331
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37266 c 36861 g 37268
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94754. .106759
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81573. .94653
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64004. .73106
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57083. .63903
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49696 ...56982
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43915. .49595
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37690. .43814
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17567. 19747
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/clone_lib="RPCI-11 Human
1. .1283
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/db_xref="taxon:9606"
/chromosome="17"
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73207. .81472
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19848. .22997
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10925. .13710
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4261. .6377
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1384. .2931
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135105. .151780
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Pred. No. 0;
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                                                                                                                                         aaaatgagggtggaggtgggaataggatctcgaggagactattggcatatgattccaagg
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ACCESSION
VERSION
KEYWORDS
SOURCE
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AC073954/c
                        REFERENCE
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                                                                                                               Homo sapiens chromosome 1
SEQUENCE, 34 unordered pi
AC073954
AC073954, 3 GI:10998993
HTG; HTGS_PHASE1; HTGS_DR
      1 (bases 1 to 177744)
Waterston, R.H.
                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                              Homo sapiens
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JOURNAL
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Sequencing vector: plasmid; 0%
Sequencing vector: plasmid; 0% of reads
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 155679 bases at least 040
Consensus quality: 163329 bases at least 020
Consensus quality: 163329 bases at least 020
Insert size: 18500; agarose-fp
Insert size: 18559; sum-of-contigs
Quality coverage: 3.43 in 020 bases; sum-of-contigs
Quality coverage: 3.43 in 020 bases; sum-of-contigs
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Unpublished
2 (bases 1 to 177744)
Waterston, R. H.
Direct Submission
Submitted (07-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
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10884. .12763
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44110. .47829
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25800 . 28333
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17466. 19992
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15482. .17365
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12864. .15381
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39983. .44009
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20093. .23512
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47930. .53768
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53869. .60215
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157290. .166822
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86053. .93510
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117891. .126044
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|09896. .117790
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pred. No. 1.7e-195;
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FEATURES

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109896 117791 117891 100819 109796

78983: gap of u 86552: gap of u 93510: contig o 93510: gap of u 100718: contig o 110718: contig o 110790: contig o 111790: contig o 111790: contig o 117790: contig o 117800: gap of u 126044: gap of u 126144: gap of u 134542: gap of u 14563: contig o 145763: gap of u 157189: contig o 145763: gap of u 157189: gap of u 166822: gap of u 166822: gap of u 166822: gap of u 166922: gap of u 177744: contig o 166822: gap of u 166822: gap

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                 l (bases 1 to 642)
Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,
Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.
Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P.,
Hamersma,H., Beighton,P. and Mulligan,J.T.
Bone Dysplasia Sclerosteosis Results from Loss of the SOST
Product, a Novel Cystine Knot Containing Protein
Am. J. Hum. Genet. 68 (3), 577-589 (2001)
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AF326742
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                                                                                                                                       African green monkey. Cercopithecus aethiops
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            agcgccaaagccaaccaggccgagctggagaacgcctactag
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GGGGCCAAAGCCAATCAGGCCGAGCTGGAGAACGCCTACTAG
                                                              gacttcgggaccgaggccgctcggccgcagaagggccgggaagccgcgcgggcccgg
                                                                                                                                                                 CGCGGCAAGTGGTGGCGCCCGAGTGGGCCCGACTTCCGCTGCATCCCGACCGCTACCGC
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                                                GACTTCGGTCCCGAGGCCGCTCGGCCGCAGAAGGGCCGGAAGCCGCGCGCCCGCGCCCCGG
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Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,
Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T.,
Hamersma,H., Beighton,P. and Mulligan,J.T.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="sclerostin"
/product="sclerostin"
/product="sclerostin"
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EPPPELENNKTMNRAENGGRPDHHPFETKDVSEYSCRELHFTRYVTDGPCRSARPVTE
LVCSGQCGPARLLPNAIGRGKWMFSGPDFRCIPDTYRAQRVQLLCPGGAAPRARKVR
LVASCKCKTLTRFHUGSELKDFGPEAARPQKGRKPRPRARGAKANQAELENAY"
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Location/Qualifiers
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/db_xref="taxon:9534"
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Pred. No. 5.1e
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ccgcagcgccaagccggtcaccgagctggtgtgtcccggccagtgcggcccggcgcct
                                                          GACCATGAACCGGGCCGAGAACGGAGGCAGACCCCCCCCATCCTTATGACACCAAAGA
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1 (bases 1 to 674)

1 (bases 1 to 674)

Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,

Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.,

Kovacevich,B.R., Sidilett,L., Colbert,T., Tacconi,P., Galas,

Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P., Galas,

Hamersma,H., Beighton,P. and Mulligan,J.T.

Bone Dysplasia Sclerosteosis Results from Loss of the SOST Gene

Product, a Novel Cystine Knot-Containing Protein

Am. J. Hum. Genet. 68 (3), 577-589 (2001)
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Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,
Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.,
Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P., Ga
Hamersma,H., Beighton,P. and Mulligan,J.T.
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AF326741
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Submitted (07-DEC-2000) Genomics,
220th St. SE, Bothell, WA 98021, U
Location/Qualifiers
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/product="sclerostin"
/produc
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/strain="Sprague-Dawley"
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                           Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 155679 bases at least Q40
Consensus quality: 153329 bases at least Q30
Consensus quality: 166780 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 183559; sum-of-contigs
Ouality coverage: 3.29 in Q20 bases; sum-of-contigs
Ouality coverage: 3.43 in Q20 bases; sum-of-contigs
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Submitted (07-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Mammalia; Eutheria; Primates;
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consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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126145. .134442
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78984. .85952
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Location/Qualifiers
1. .177744
                                                                                                                                                                vector_side:left"
                                                                                                                                                                                                                                          /note="assembly_name:Contig52"
66578. .71476
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60316. .66477
                                                                                                                                                                                                                                                                                                      /note="assembly_name:Contig49"
47930..53768
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44110. .47829
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39983. ,44009
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20093. 23512
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145764. .157189
                               /note="assembly_name:Contig61"
134543. .145663
                                                                                              100819. .109795
/note="assembly_name:Contig58"
109896. .117790
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/note="assembly_name:Contig63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_name:Contig42"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="assembly_name:Contig39"
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                                                                                                                 note="assembly_name:Contig57"
.00819. .109795
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Sabo, P.J.,

Galas,

SOST

.W., Sabo, P.J.,

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KEYWORDS
SOURCE
ORGANISM
                                                                                     DEFINITION
ACCESSION
VERSION
                                                                                                                                RESULT 1
AF326740
LOCUS
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628; Conservative
                                                                               Mus musculus sclerostin
AF326740
AF326740.1 GI:13161000
Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 638)
                                          house mouse.
Mus musculus
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/note="assembly_name:Contig64"
166923. .17744
/note="assembly_name:Contig65"
a 43012 c 43431 g 43839 t
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              Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                          cgcggcaagtggtggcgacctagtgggcccgacttccgctgcatccccgaccgccaccgc
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                                          CGCGTGAAGTGGTGGCCCCGAACGGACCGGATTTCCGCTGCATCCCGGATCGCTACCGC
                                                                                                                                                                                                                     CGCGAGCTGCACTACACCCGCTTCCTGACAGACGGCCCATGCCGCAGCGCCAAGCCGGTC
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Kovacevich, B.R., Proll, S., Skonier, J.E., Zhao,
Fu, Y.H., Alisch, R.S., Gillett, L., Colbert, T.,
Hamersma, H., Beighton, P. and Mulligan, J.T.
Direct Submission
Submitted (07-DEC-2000) Genomics, Celltech Chi
220th St. SE, Bothell, WA 98021, USA
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11179006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/product="sclerostin"
/protesh_id="aak13455.1"
/protesh_id="aak13455.1"
/db_xref="GI:13161023"
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ASCKCKRLTRFHNQSELKDFGPETARPQKGRKPRPGARGAKANQAELENAY"
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1. .638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="1295v/J"
/db_xref="taxon:10090"
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Pred. No. 1.2e-86;
0; Mismatches 75;
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Zhao, L., Sabo, P.;
t, T., Tacconi, P.,
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agaatgatgccacggaaatcatccccgagctcggagagtaccccggagcctccaccggagc 195
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                                                                    T---GAACAACAAGACCATGAACCGGGCGGAGAACGGAGGGAGAGACCTCCCCACCACCACCCCT
                                                                                  tggagaacaacaagaccatgaaccgggcggagaacggagggcggcctccccaccacccct
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                                                                                                                                     AGAATGATGCCACAGAAATCATCCCCGAGCTGGGCGAGTACCCCGAGCCTCTGCCAGAGC
                                                                                                                                                                                                      500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 532)

Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,

Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.,

Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P., Galas,D.

Hamersma,H., Beighton,P. and Mulligan,J.T.

Direct Submission

Submitted (07-DEC-2000) Genomics, Celltech Chiroscience Inc., 1631

220th St. SE, Bothell, WA 98021, USA
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11179006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF326738 532 bp mRNA
Bos taurus sclerostin mRNA,
AF326738 GI:13161016
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                                                                                                                                                                                                                      Similarity
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GRKLRPAARGTKASRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
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Pred. No. 4.7e
0; Mismatches
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No. 4.7e-80;
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-~ni.P., Galas,D
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E. 1 (bases 1 to 17423)

S. Brunkow, M.E., Gardner, J.C., Van Ness, J., Paeper, B.W., Sabo, P.J., Svoacevich, B.R., Proll, S., Skonier, J.E., Zhao, L., Sabo, P.J., Fu, Y.H., Alisch, R.S., Gillett, L., Colbert, T., Tacconi, P., Gal Hamersma, H., Beighton, P. and Mulligan, J.T.

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Mus musculus sclerostin
AF326737
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Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,
Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.,
Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P.,
Hamersma,H., Beighton,P. and Mulligan,J.T.
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/db_xref="taxon:10090"
/chromosome="11"
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Sequence split into 5
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Continuation (3 of 5) o
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Mus muscullus chromosome
SEQUENCE, 34 unordered p
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus chromosome 11, clone RP23-346P7
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----- Genome Center
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Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                          Center project Information
                                                                                                                                                                                            Center clone name:
                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@genome
                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number will be preserved.
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                                                                              107500 107599: gap of 107600 115731: cont
                                                                                                                                                          91795 91794: gap of 100 bp
91795 99208: contig of 7414 bp in
99209 99308: gap of 100 km
                                                                                                                                                                                                                                                                                                                                       59531 64373; contig of 4843 bp in length 64374 64473; gap of 100 bp 64474 70503; contig of 6030 bp in length 70504 70603; gap of 100 bp 70604 77829; contig of 7226 bp in length 77830 7829; gap of 100 bp 77830 7829; contig of 7226 bp in length 77830 7829; gap of 100 bp
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14684: contig of 1992 k

185 14784: gap of 100 bp

185 17163: contig of 2379 bp

64 17263: gap of 100 hr

19900: The state of 100 hr
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13 29512: contig of 3301 bp

13 29512: gap of 100 bp

13 32991: contig of 3479 bp

12 33091: gap of

2 36913: ---
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3065; m
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25011: contig of 2857 l
12 26111: gap of 100 hr
2 29412: con+'
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5 59430: contig of 5
11 59530: gap of 10
11 64373: contig of 4
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31 40980: gap of 10
45015: contig of 4
6 45115: gap of 10
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10198: gap of 100 bp
12592: contig of 2394 bp in lenath
12692: gap of 100 b-
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20000: gap of 100 bl
23054: contig of 3054
23154: gap of 100 bl
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4405: gap of 1
5983: contig of
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107499: contig of 8191
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85976: contig of 8047 bp in length
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134080 144631; contig of 10552 bp
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144732 159118; contig of 14387 bp
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172538 200727: contig of 28190
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45116. .50321
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99309. .107499
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/map="11"
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tive 0; Mismatches 68; Indels 0; G
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Search completed: November 8, 2001, 23:49:26 Job time: 16136 sec

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Brunkow, M.E., Gardner, J.C., Van Ness, J., Paeper, B.W., Kovacevich, B.R., Proll, S., Skonier, J.E., Zhao, L., Sabo, P.J. Fu, Y.H., Alisch, R.S., Gillett, L., Colbert, T., Tacconi, P., GHamersma, H., Beighton, P. and Mulligan, J.T.
Bone Dysplasia Sclerosteosis Results from Loss of the SOST Product, a Novel Cystine Knot-Containing Protein Am. J. Hum. Genet. 68 (3), 577-589 (2001)
                  Submitted (07-DEC-2000) Genomics, Celltech Chiroscience Inc., 220th St. SE, Bothell, WA 98021, USA Location/Qualifiers
                                                          Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,
Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.,
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                                                                                                                                                       Compositions and methods for the treatment Patent: WO 0075317-A 19 14-DEC-2000; Genentech, Inc. (US) Location/Qualifiers 1. .2329
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Botstein, D.A., Goddard, A., Gurney, A.L., Smith, V., Watanabe, C.
Wood, W.I.
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Submitted (22-DEC-2000) Medical
Universiteitsplein 1, Antwerp B
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Increased bone density in sclerosteosis is due to the deficie a novel secreted protein (SOST)
Hum. Mol. Genet. 10 (5), 537-543 (2001)
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Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B. Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacc Hamersma,H., Beighton,P. and Mulligan,J.T. Bone Dysplasia Sclerosteosis Results from Loss of Product, a Novel Cystine Knot-Containing Protein 11.700.
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Hamersma, H., Beighton, P. and Mulligan, J.T.
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1718	aagagcagcatccctcccccgacccatagccatgttttaaagtcaccttccgaagag	1659	Qy
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698 15369	cgcgcccggagcgccaaagccaaccaggccgagctggagaacgcctactagagcccgccc	639 15310	Db Oy

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	ORGANISM REFERENCE AUTHORS TITLE JOURNAL	RESULT 5 ACO03098/c LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE	Qy 2259 t Db 16930 T	Qy 2199 t pb 16870 T	Qy 2139 t bb 16810 T	Qy 2079 c pb 16750 c	Qy 2019 t Db 16690 T	Qy 1959 g Db 16630 G	Qy 1899 t Db 16570 T	Qy 1839 c Db 16510 C	Qy 1779 g pb 16450 G	pb 16390 G
2 (bases 1 to 94752) 2 (bases 1 to 94752) Birren, B., Fasman, K., McKernan, K., Munro, C., Nusbaum, C., Richardson, P., Lander, E., Baldwin, J., Barna, N., Cantu, C., Chang, A., Cooke, P., Daly, M.J., Devon, K., Dewar, K., Durette, B., Forrest, C., Gage, D., Gensheimer, S., Geraigery, K., Gilmartin, T., Hagos, B., Halphen, I., Harris, K., Howland, J.C., Huang, J., Hui, L., Jacotot, L., Kirby, A., Lane, M., MacKenzie, J., Marquis, N., McDermott, J., Molla, M., Morrow, J., Nachman, A., Naylor, J., O'Connor, T., Olotu, A., Peterson, K., Roberts, D., Rollins, G., Sarnaik, A., Shiu, P., Shyam, R., Stilwell, J., Stone, C., Strickland, C., Sydney, K., Tang, L., Zemtseva, I. and Zody, M. Direct Submission Submitted (10-NOV-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 94752) Birren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Barren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Birren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Barren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Barren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Barren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Barren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Barren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Barren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Barren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Barren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Barren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Barren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Barren, B., Fasman, K., McKernan, R., Barren, B., Barren, M., Barren, M., Barren, M., Barren, B.,		AC003098 94752 bp DNA PRI 29-JAN-1998 Homo sapiens chromosome 17, clone HRPC905N1, complete sequence. AC003098 AC003098.1 GI:2822155	tccagagacattgttaataaagacaatgaatcatgaccgaaag 2301 	cottgtagagaatgacaatgttaatattgotttatgaattaacagtotgttottocagag 2258 	tttttaaagagttaagttacatatttattttctcacttaagttatttat	tggtcgtttttttggcaattcttccacgtgggacttgtccacaagaatgaaagtagtgg 2138 	ttaattyttaaaaaaaaagttttaaacagaaycacatyacatatyaaaycctycayya 2078 	gccacccaaaaatetttttgaaaatcatttccagaccacctettactttctgtgtagttt 2018 	attgggggaaaaactacaagtgctgtacatatgctgagaaactgcagagcataatagct 1958 	etagaaaacagettettaetgetettaeatgtgatggeatatettaeaetaaaagaatat 1898 	gaccagcacatccettttgagacaccgccttctgcccaccactcacggacacatttctgc 1838 	

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Submitted (29-JAN-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jan 29, 1998 this sequence version replaced gi:2665504.
The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.
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                                                                                                                                                                                                                                                                                      ccgcctctggggccgcctacctttgctggtcccacttcagaggaggcagaaatggaagca
                                                                                                                                                                                                   gtgaaaggttcaaggacactggccttgcaggcccgagggagcagccatcacaaactcaca
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                                                                                                                                                                                                                                                                                                                                                                                                    gacatatitacggctgacaaactcctggaagaagctatgctgcttccccagcctggcttcc
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gccacccaaaaatctttttgaaaatcatttccagacaacctcttactttctgtgtagttt
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                                                                                                                                                   gaccagcacatcccttttgagacaccgccttctgcccaccactcacggacacatttctgc
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Center project name: L7949 Center clone name: 209_M_4

Project Information

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SOURCE
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Karatas, A.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, M., Naylor, J., Norman, C.H., O'Connort, T., O'Donnell, P.,
O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
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                                                                                                                                                                                                                                                                         Submitted (18-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 22, 2000 this sequence version replaced gi:8920653. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, W., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand, Biorson, Grand, B., Grand, G., G., Grand, G., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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1 (bases 1 to 151780)
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                                                                                              Center code: WIBR
                                          Web site:
                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zainoun, J., Zimmer, A. and Zody, M.
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sequence_submissions@genome.wi.mit.edu
                                          http://www-seq.wi.mit.edu
                                                                                                                                                                                         Genome Center
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17
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NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be preserved
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64004 73106
73107 73206: ga
73207 81472
81473 81572: ga
81573 94653
94654 94753: ga
94754 106759
106760 10859: o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13; M77815; 94% of reads Sequencing vector: Blasmid; n/a; %-0.f%% of reads Sequencing vector: Plasmid; n/a; %-0.f%% of reads 6.15883306320908Chemistry: Dye-terminator Big Dye
                                                                                    100 bp 10 118633: contig of 11774 bp in 118634 118734; gap of 100 bp 118734 135004: contig of 100 bp 135005 135005
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135105 151780;
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37589: contig of 5158 k
37689: gap of 100 bp
43814: contig of 6125 k
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22997: contig of 3150 k
23097: gap of 100 bp
26840: contig of 3743 k
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3031: gap of 100 bp
4160: contig of 1129
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106759: contig of 12006 bp in
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81472: contig of 8
1572: gap of 10
94653: contig of 1
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56982: contig of 7287 k
100 bp
63903: contig of 6821 k
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49595: contig of 5681 k
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3: gap of 100 bp
2931: contig of 1548 bp in length
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06: contig of 9103 k
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1478	tctgacagccaaagatgaaaaacagaaaaaaaaaaaaagtaaagagtctatttatggct	y 1419	õ
1418	tgcagttgcattgattcagtgccaaggtcacttccagaattcagagttgtgatgctctct	y 1359	Qy
113250		b 113191	Db
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112290		b 112231	Db
112230		b 112171	Dβ

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                                                                 Homo sapiens chromosome 17 clone SEQUENCE, 34 unordered pieces. ACO73954.3 GI:10998993
HTG; HTGS_PHASE1: HTGG
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 177744)
                                             Homo sapiens
                                                                                                                   RP11-147C10,
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                       Hominidae;
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WORKING DRAFT
                                  Euteleostomi;
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submitted (07-JUL-2000) Genome
University School of Medicine,
MO 63108, USA
On Oct 25, 2000 this sequence v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemistry: Dye-primer ET; 100% of reads chemistry: Dye-terminator Big Dye: 0% of reads Assembly program: Phrap: version 0.990319 consensus quality: 155679 bases at least Q40 Consensus quality: 163329 bases at least Q30 Consensus quality: 166780 bases at least Q20 Insert size: 185000; agarose-fp Insert size: 18559; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 3.29 in Q20 bases; agarose-fp Quality coverage: 3.43 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
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Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence of Homo sapiens clone Unpublished 2 (bases 1 to 177744)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                             as soon as it is available and the accession number be preserved.
  ----- Summary Statistics -----
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86053. .93510
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Pred. No. 5.6e-195;
0; Mismatches 31; Indels 4; Ga
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66577; gap of unknown le
71476; contig of 4899 bp
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71476; contig of 7307 bp
71883; contig of 7307 bp
78883; contig of 6969 bp
86052; gap of unknown le
85952; contig of 7458 bp
93610; gap of unknown le
93610; gap of unknown le
100718; contig of 7108 bp
100818; gap of unknown le
100718; contig of 8977 bp
109895; gap of unknown le
117790; contig of 8978 bp
117790; contig of 8154 bp
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126144; gap of unknown le
126144; contig of 8154 bp
134442; contig of 8128 bp
134542; gap of unknown le
134543; gap of unknown le
134543; gap of unknown le
134563; contig of 11121 b
145763; gap of unknown le
157189; contig of 11426
157189; contig of 13458
166922; gap of unknown le
167289; gap of unknown le
167289; gap of unknown le
167244; contig of 10822 b

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source

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23613. .25699

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      AF326742 Cercopithecus AF326742 AF326742.1 GI
                                                                                             African green monkey.
Cercopithecus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                Cercopithecinae; Cercopithecus.
1 (bases 1 to 642)
(bases 1 to
                                                                                                                                             GI:13161028
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aethiops
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                                                                                               Vertebrata; Euteleostomi;
i; Cercopithecidae;
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                                                            Sabo, P.J.,
                                                    Galas, D.,
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                                                              gacttcgggaccgaggccgctcggccgcagaagggccggaagccgcgggcccgcgcgg
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                                                 GACTTCGGTCCCGAGGCCGCTCGGCCGCAGAAGGCCGGAAGCCGCGGCCCCGCGCCCGG
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Submitted (07-DEC-2000) Genomics,
220th St. SE, Bothell, WA 98021,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brunkow, M. E., Gardner, J.C., Van Ness, J., Paepe
Kovacevich, B.R., Proll, S., Skonier, J. E., Zho,
Fu, V. H., Alisch, R. S., Gillett, L., Colbert, T.,
Hamersma, H., Beighton, P. and Mulligan, J.T.
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nilarity 96.9%;
Conservative
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EPPPELENNKTMNRAENGGREPHHFFEYKDVSEYSCRELHFTRYVTGGFCRSAKEVTE

LVCSGQCGPARLLPNAIGRGKWHRPSGPDFRCIPDRYRAQRVQLLCPGGAAPRARKVR

LVASCKCKRLTRFHMQSELKDFGFBAARPQKGKKPRPRARGAKANQAELENAY"

228 c 210 g 91 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="sclerostin"
/protein_id="AAK13457.1"
/db_xref="GI:13161029"
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/db_xref="taxon:9534"
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Pred. No. 4.1e-107;
0; Mismatches 20;
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USA
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                                                                                                                        AGAAATCATCCCGGGACTCAGAGAGTACCCAGAGCCTCCTCAGGAACTAGAGAACAACCA
                                                                                                                                                                                            ggaaatcatccgcgagctcggagagtaccccgagcctccaccggagctggagaacaacaa
                                                                                                                                                                                                                                                                                                                                          GACCATGAACCGGGCCGAGAACGGAGGCAGACCCCCCCACCATCCTTATGACACCAAAGA
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Rattus norvegicus sclerostin
AB326741
AF326741.1 GI:13161075
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Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.,
Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P., Galas,D.,
Hamersma,H., Beighton,P. and Mulligan,J.T.
Bone Dysplasia Sclerosteosis Résults from Loss of the SOST Gene
Product, a Novel Cystine Knot-Containing Protein
Am. J. Hum. Genet. 68 (3), 577-589 (2001)
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Brunkow, M.E., Gardn
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Rattus norvegicus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (07-DEC-2000) Genomics, 220th St. SE, Bothell, WA 98021,
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Kovacevich, B.R., Proll, S., Skonier, J.E., Zhao, L., Sabo, P.J.,
Fu, Y.H., Alisch, R.S., Gillett, L., Colbert, T., Tacconi, P., Galas, D.,
Hammersma, H., Beighton, P. and Mulligan, J.T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Godon_start=1
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/protein_id="AaK13456.1"
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LVASCKCKLTTRFHNQSELKDFGPETARPQKGRKPRPRARGAKANQAELENAY"
LVASCKCKRLTRFHNQSELKDFGPETARPQKGRKPRPRARGAKANQAELENAY"
240 c 208 g 98 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     23.2%;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                  Score 533; DB 94;
Pred. No. 2.4e-92;
0; Mismatches 80;
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Sciurognathi; Muridae
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                                                                                                     253
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TITLE
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                          Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 155679 bases at least Q40
Consensus quality: 153329 bases at least Q30
Consensus quality: 166780 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 18559; sum-of-contigs
Quality coverage: 3.29 in Q20 bases; sgarose-fp
Quality coverage: 3.43 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                Direct Submission Submitted (07-UUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Oct 25, 2000 this sequence version replaced gi:9186849.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 177744) Waterston, R.H.
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1 (bases 1 to 177744)
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HTG; HTGS_PHASE1; HTGS_DRAFT
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'working draft'
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    karyota; Metazoa; Chordata;
mmalia; Eutheria; Rodentia;
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                                                                                      CGCGTGAAGTGGTGGCGCCCGAACGGACCGGATTTCCGCTGCATCCCGGATCGCTACCGC
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2 (bases
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Brunkow, M.E., Gardner, J.C., Van Ness, J., Paeper, B.W.,
Brunkow, M.E., Froll, S., Skonier, J.E., Zhao, L., Sabo, P.J.,
Kovacevich, B.R., Proll, S., Skonier, J.E., Zhao, L., Sabo, P.J.,
Fu, Y.H., Alisch, R.S., Gillett, L., Colbert, T., Tacconi, P., Ga
Hamersma, H., Beighton, P. and Mulligan, J.T.
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/ssckckklttehagevp
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/ssckckkltte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SE, Bothell, WA 980
Location/Qualifiers
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87.4%;
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Pred. No. 2.1e-86
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638;

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414

467 354 407 294 347 234 287 174 227

587

δõ ď Qy 밁 Qγ Дb Ş ф δÃ 망 γQ 엉 γQ

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Best Local
                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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                             256
                                                            61
               | ttgagaccaaagacgtgtccgagtacagctgccgcgagctgcacttcacccgctacgtga
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                                                                                                                                          agaatgatgccacggaaatcatccgcgagctccggagagtaccccggagcctccaccggagc
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TTGAGACCAAAGACGCCTCCGAGTACAGCTGCCGGGAGCTGCACTTCACCCGCTACGTGA
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                                                                                                                         AGAATGATGCCACAGAAATCATCCCCGAGCTGGGCGAGTACCCCGAGCCTCTGCCAGAGC
                                                                                                                                                                                         499;
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1 (bases 1 to 532)

1 (bases 1 to 532)

Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,
Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.,
Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.,
Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P., Galas,
Hammersma,H., Beighton,P. and Mulligan,J.T.

Bone Dysplasia Sclerosteosis Results from Loss of the SOST Gene
Product, a Novel Cystine Knot-Containing Protein

T Hum. Genet. 68 (3), 577-589 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
AF326738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (07-DEC-2000) Genomics, Celltech Chiroscience 220th St. SE, Bothell, WA 98021, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,
Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J
Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P., (
Hammersma,H., Beighton,P. and Mulligan,J.T.
Direct Submission
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Mammalia; !
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                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                     95
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GRKLRPRARGTKASRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Bos taurus"
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<1. .>532
                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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93
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Pred. No. 1.6e-79;
0; Mismatches 33
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AF326737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gcccggcgcgcctgctgcccaacgccatcggccgcggcaagtggtggcgacctagtgggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Recul-
Mammalia; Eutheria; Rodentia, ...

1 (bases 1 to 17423)

Brunkow, M.E., Gardner, J.C., Van Ness, J., Paeper, B.W.,
Kovacevich, B.R., Proll, S., Skonier, J.E., Zhao, L., Sabo, P.J.,
Kovacevich, B.R., S., Gillett, L., Colbert, T., Tacconi, P., Galas, I.,
Fu, Y.H., Beighton, P. and Mulligan, J.T.
Bone Dysplasia Sclerosteosis Results from Loss of the SOST Gene
Product, a Novel Cystine Knot-Containing Protein

4 Hum. Genet. 68 (3), 577-589 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGGCGCGCGCGCGCGCGCAAGGTGCGCCTGGTGGCCTCGTGCAAGTGCAAGCGCC
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                                                                                                                                                                                                                                                                                                                                                           Submitted 220th St.
                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 17423)
Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,
Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.:
Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P.,
Hamersma,H., Beighton,P. and Mulligan,J.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus sclerostin
AF326737
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join(8036. .8249,10742.
                                                                                                                                                                                                                            join(<8036. .8249,10742.
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AC068782_3
AC068782_4
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Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collynore, A.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Hehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                        pirect Submission
Submitted (22-0CT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on May 25, 2000 this sequence version replaced gi:7329383.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 200727)
Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
                                                                                                                         Center project name: L3205
Center clone name: 346_P_7
                                                                                                                                                                                         Contact: sequence_submissions@genome.wi
                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.
                                                                                                                                                                                                                                                                       Center code: WIBR
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                                                                                                         85977 86076; gap of 10
86077 91694; contig of 5
91695 91794; gap of 10
91795 99208; contig of 7
99209 99308; gap of 10
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8322: contig of 2239 l
8323 8422: gap of 100 bp
8423 1098: contig of 1676 b
10099 10198: gap of 100 bp
10199 12592: contig of 2394 b
12593 12692: gap of 100 bp
12593 12692: gap of 100 bp
12693 14684: contig of 1992 b1
14685 14784: gap of
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4306 4405: gap of 100 bp
4406 5983: contig of 1578
5984 6083: gap of 100 bp
6084 8322: contig
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14785 17163; contig of 2
17164 17263; gap of 10
17264 19900; contig of 2
19901 20000; gap of 10
20001 23054; contig of 3
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1092 1191: gap of 100 bp
1192 3065: contig of 1874 bp in length
3066 3165: gap of 100 bp
3166 4305: contig of 1140 bp in length
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0603: gap of 1)
77829: contig of 7929: gap of 1
85976: contig of 6
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50321: contig of 5206 bp
0421: gap of 100 bp
54284: contig of 3863 bp
4384: gap of 100 bp
55430: contig of 5046 bp
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36913: contig of 17
7013: gap of 11
40880: contig of 10
0980: gap of 11
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64373: contig of 10
1473: gap of 10
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115731: CC
1831
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8423. 10098
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77930. .85976
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70604. .77829
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1192. .3065
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/db_xref="taxon:10090"
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54474. .70503
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34079: gap of 100 bp
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44731: gap of
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Copyright (c) 1993 - 2000 Compugen Ltd.
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em_esthum22:
em_esthum25:
em_esthum25:
em_esthum25:
em_esthum26:
em_esthum27:
em_esthum27:
em_estin1:
em_estin1:
em_estin2:
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190 9) csctll:*
191 9b.sctll:*
192 9b.htc:*
192 9b.htc:*
193 em_gs.lma*
193 em_gs.lma*
194 em_gs.lma*
195 em_gs.lma*
196 em_gs.lma*
200 em_gs
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9b_est48: *
9b_est51: *
9b_est51: *
9b_est51: *
9b_est53: *
9b_est54: *
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9b_est56: *
9b_est57: *
9b_est60: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1 gaggaccgagtqccc
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Copyright (c) 1993 - 2000 Compugen
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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length: 2000000000
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em_estom2: em_estov1: em_estov1: em_estp11: em_estp12: em_estp14: em_estp16: em_estp17: em_estp16: em_estp10: em_est

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gb_est45:*
gb_est46:*

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9b_est511;
9b_est548;
9b_est548;
9b_est554;
9b_est554;
9b_est554;
9b_est556;
9b_est566;
9b_est660;
9b_est60;
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being and is derived by analysis of the total score distribution. have a ing printed,

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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	668 709:: 711:: 712:: 713:: 714:: 715:: 716:: 71		
gb_pr2; gb_pr3; gb_pr4; gb_pr5; gb_pr5; gb_pr5; gb_pr7; gb_pr9; gb_pr9; gb_r01; gb_r01; gb_r01; gb_r01; gb_pr9; gb_pr9; gb_pr9; gb_pr9; gb_pr9; gb_pr9; gb_pr9;	b_htg90; b_htg11 b_htg13 b_htg13 b_htg14 b_htg16 b_htg16 b_htg16 b_htg17 b_htg17 b_htg17 b_htg18 b_htg19 b_htg21 b_htg23 b_htg23 b_htg23	b_sts3: b_sy:* b_un:* b_un:* b_vi1:* b_vi2:** b_htg1:* b_htg3: b_htg4: b_htg5: b_htg6: b_htg6:	em_ov:* em_ph:* em_ph:* em_pl:* em_ro:* em_sy:* em_un:* em_un:* em_vi:* qb_sts2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		% Query				
No.	Score		Ė	DB BG	ID	Description
₽	532	100.0		7	AF326738	AF326738 Bos tauru
2	467.8	87.9		89	AF331844	AF331844 Homo s
ω	467.8	87.9	2323	89	AF326739	AF326739 Homo sapi
4	467.8	87.9		9	AX056687	AX056687 Sequenc
σı	461.4	86.7		89	AF326742	AF326742 Cercop
0	424.6	79.8		94	AF326741	AF326741 Rattus
7	414.2	77.9		94	AF326740	AF326740 Mus mu
œ	375.2	70.5		89	AF326736	AF326736 Homo s

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REFERENCE
AUTHORS
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     FEATURES
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Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,

Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.

Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P., (Hamersma,H., Beighton,P. and Mulligan,J.T.
           Direct Submission
Submitted (07-DEC-2000) Genomics,
220th St. SE, Bothell, WA 98021,
                                                                                                                                                              AF326738 532 bp mRNZ
Bos taurus sclerostin mRNA,
AF326738
                                                                                                                               Bos taurus
Eukaryota;
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AE005746
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5 AC080138
5 AC073809
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                   Celltech Chiroscience
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AL059024 Homo sapi
AL059024 Homo sapi
AL048395 T3 end of
AC010827 Homo sapi
AC024907 Homo sapi
AC024912 Sequence
AL438395 T3 end of
AC027562 Homo sapi
AC024319 Sequence
AL438395 T3 end of
AC027562 Homo sapi
AC068018 Homo sapi
AC068018 Homo sapi
AL356002 Homo sapi
AL356002 Homo sapi
AL429856 clone BA0
AJ133131 Myxococcu
AL079308 Streptomy
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Balemans, W., Ebeling, M., Patel, N., va
Dioszegi, M., Lacza, C., Wuyts, W., van
Paes-Alves, A.F., Hill, S., Bueno, M., R
Dikkers, F.G., Stratakis, C., Lindpaint
Foernzler, D. and Van Hul, W.
                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 2296)
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AF331844
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/translation="NNDATELIPELGEYPEPLPELPULP"
/translation="NNDATELIPELGEYPEPLPELPULP"
/translation="NNDATELIPELGEYPEPLP"
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/db_xref="taxon:9913"
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                               Lindpaintner, K.,
                                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                                                                                    complete
                                                                                                     van Hul, E.,
                                                 van Hul,E., Olson,P.,
n den Ende,J., Willems,P.,
Ramos,F.J., Tacconi,P.,
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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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gb_pat2:*
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gb_ph::*
gb_pl1::*
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gb_pl4::*
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9b_ba2: *
9b_ba3: *
9b_in1: *
9b_in2: *
9b_in3: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

								Result
œ	7	σ	U	4	ω	2	1	ult No.
407.4	424.6	530	536.2	536.2	536.2	556	674	Score
60.4	63.0	78.6	79.6	79.6	79.6	82.5	100.0	Query Match
17423	532	642	2329	2323	2296	638	674	Query Match Length DB
94	7	89	9	89	89	94	94	i
AF326737	AF326738	AF326742	AX056687	AF326739	AF331844	AF326740	AF326741	ID
AF326737 Mus muscu	AF326738 Bos tauru	AF326742 Cercopith	AX056687 Sequence	AF326739 Homo sapi	AF331844 Homo sapi	AF326740 Mus muscu	AF326741 Rattus no	Description

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AF326741 674 k
Rattus norvegicus s
AF326741
AF326741.1 GI:1318
                                                               2 (bases 1 to 674)
Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,
Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.,
Fu,Y.H., Allsch,R.S., Gillett,L., Colbert,T., Tacconi,P., Galas,
Hamersma,H., Beighton,P. and Mulligan,J.T.
                                                                                                                                           Brunkow, M.E., Gardner, J.C., Van Ness, J., Paeper, B.W., Kovacevich, B.R., Proll, S., Skonier, J.E., Zhao, L., Sabo, P.J., Fu, Y.H., Alisch, R.S., Gillett, L., Colbert, T., Tacconi, P., Galas, Hamersma, H., Beighton, P. and Mulligan, J.T. Bone Dysplasia Sclerosteosis Results from Loss of the SOST Gene Product, a Novel Cystine Knot-Containing Protein Am. J. Hum. Genet. 68 (3), 577-589 (2001)
                                                                                                                                                                                                                                                                                 Rattus norvegicus
Eukaryota; Metazoa;
                          Submitted (07-DEC-2000) Genomics, Celltech 220th St. SE, Bothell, WA 98021, USA
                                                       Direct Submission
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                           (bases 1 to 674)
Location/Qualifiers
1. 674
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Sciurognathi; Muridae; Murinae;
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complete cds
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AL438395 T3 end of
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AC068018 Homo sapi
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LVASCKCKRLTRFHNQSELKDFGPETARPQKGRKPRPRARGAKANQAELENAY"
a 240 c 208 g 98 t
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360 360 300 300 240 240

180 180 120 120 60

PUBMED REFERENCE AUTHORS

JOURNAL TITLE

11179006

FEATURES

source

28-FEB-2001

660 660 600 540 540 480 480 420

REFERENCE AUTHORS

Rattus.

VERSION KEYWORDS SOURCE DEFINITION ACCESSION

ORGANISM

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2: 9b_ba2:*
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6: 9b_pat1:*
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10: 9b_pat1:*
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15: 9b_pl1:*
16: em_ba1:*
17: em_ba1:*
18: em_htgo_in
20: em_htgo_in
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40: em_hum::*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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em_hum2:*
em_hum3:*
em_hum4:*
em_hum5:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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0000 7	.7423 94	2329 9			642 8	674 94	638 94	Length DB
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Continuation (3 of	AF326737 Mus muscu	AX056687 Sequence	AF326739 Homo sapi	AF331844 Homo sapi	AF326742 Cercopith	AF326741 Rattus no	AF326740 Mus muscu	Description

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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murii
1 (bases I to 638)
1 (bases I to 638)
1 (bases I, Gardner, J.C., Van Ness, J., Paeper, B.W.,
Kovacevich, B.R., Proll, S., Skonier, J.E., Zhao, L., Sabo, P.,
Kovacevich, B.R., S., Gillett, L., Colbert, T., Tacconi, P.,
Fu, Y. H., Alisch, R.S., Gillett, L., Colbert, T., Tacconi, P.,
Hamersma, H., Beighton, P. and Mulligan, J.T.
Bone Dysplasia Sclerosteosis Results from Loss of the SOS:
                                                                                                                                                                                                                                                       Am. J. Hu
11179006
                                                                 Direct Submission
Submitted (07-DEC-2000) Genomics,
220th St. SE, Bothell, WA 98021,
                                                                                                                                   2 (bases 1 to 638)
Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,
Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.,
Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P., Galas,
Hamersma,H., Beighton,P. and Mulligan,J.T.
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Mus musculus sclerostin
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AC055813 Homo sapi
AC053813 Homo sapi
AC073954 Homo sapi
AC073955 Homo sapi
AC079155 Homo sapi
AL050024 Homo sapi
AX071502 Sequence
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AF217189 Scrangium
AL157953 Streptomy
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X95710 Pseudorabie
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AL1429856 clone BA0
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AL143199 Homo sapi
AC084804 Mus muscu
AL438395 T3 end of
AB044709 Grylius b
L38927 Moiluscum c
AL391039 Streptomy
AC090952 Homo sapi
AC0804816 Streptomy
AC090952 Homo sapi
AL042986 Streptomy
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/protein_id="AAK13455.1"
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/db_xref="Gi:3161023"
/db_xref="Gi:3161023"
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Pred. No. 6.1e-101;
; Mismatches 0;
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REFERENCE AUTHORS

JOURNAL PUBMED

TITLE

FEATURES.

JOURNAL

REFERENCE AUTHORS

ORGANISM KEYWORDS VERSION

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LOCUS DEFINITION ACCESSION RESULT AF326740

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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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44 em_pat: *

46 em_ph: *

48 em_pt: *

48 em_to: *

48 em_to: *

49 em_sts: *

50 em_sy: *

51 em_un: *

52 em_vi: *

53 gb_sts1: *

54 gb_sts3: *

55 gb_sts3: *

56 gb_yt2: *

60 gb_htg1: *

61 gb_htg4: *

62 gb_htg4: *

63 gb_htg4: *

64 gb_htg4: *

65 gb_htg4: *

66 gb_htg1: *

70 gb_htg1: *

71 gb_htg1: *

71 gb_htg1: *

72 gb_htg1: *

73 gb_htg1: *

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78 gb_htg2: *

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99 gb_htg2: *

90 gb_htg2: *

90 gb_htg2: *

91 gb_htg2: *

92 gb_htg2: *

93 gb_htg2: *

94 gb_htg2: *

95 gb_pr1: *

96 gb_pr1: *

97 gb_htg2: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	64.4	71.9	78.4	82.6	95.5	95.5	95.5	100.0	Query Match	æ	
		532	638	674	2329	2323	2296	642	Query Match Length DB		
	89	7	94	94	9	89	89	89	DB		
	AF326736	AF326738	AF326740	AF326741	AX056687	AF326739	AF331844	AF326742	ID		SUMMARIES
	AF326736 Homo sapi	AF326738 Bos tauru	AF326740 Mus muscu	AF326741 Rattus no	AX056687 Sequence	AF326739 Homo sapi	AF331844 Homo sapi	AF326742 Cercopith	Description		55

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Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,
Brunkow,M.E., Gardner,J.C., Skonier,J.E., Zhao,L., Sabo,P.J.,
Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.,
Fu,Y.H., Allsch,R.S., Gillett,L., Colbert,T., Tacconi,P., Galas,J.
Fu,Y.H., Allsch,R.S., Gillett,L., Colbert,T., Tacconi,P., Galas,J.
Hamersma,H., Belghton,P. and Mulligan,J.T.
Bone Dysplasia Sclerosteosis Results from Loss of the SOST Gene
Product, a Novel Cystine Knot-Containing Protein
Thum. Genet. 68 (3), 577-589 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                   AF326742 (Cercopithecus a
AF326742
AF326742.1 GI
          Brunkow,M.E., Gardner,J.C., Van Ness,J., Paepo
Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,
Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T.,
Hamersma,H., Beighton,P. and Mulligan,J.T.
Direct Submission
Submitted (07-DEC-2000) Genomics, Celltech Chi
220th St. SE, Bothell, WA 98021, USA
                                                                                                                                                                                                                                                                                                                                                     African green monkey. Cercopithecus aethiops
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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AC068018
AC010827
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Zhao,L., Sabo,P.J.,
t,T., Tacconi,P., Ga
                                               Chiroscience
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M57388 Sinhav herp
X56935 Herpesvirus
AL438395 T3 end of
AC079636 Mus muscu
AC027530 Homo sapi
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GGGGCCAAAGCCAATCAGGCCGAGCTGGAGAACGCCTACTAG
                                                                                                                                                       CTGGTGGCCTCGTGCAAGTGCAAGCGCCTCACCCGCTTCCACAACCAGTCGGAGCTCAAG
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/codon_ftart=1
/product="sclerostin"
/protein_id="AaKi3457.1"
/protein_id="AaKi34
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/db_xref="taxon:9534"
1.642
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Pred. No. 4.1e-102;
; Mismatches 0;
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